Supporting Information

The Evolutionary Genomics of Grape (*Vitis vinifera* ssp. *vinifera*) Domestication

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SUPPLEMENTARY TEXT

Supplementary Methods:

Samples and sequencing: We collected leaf tissue for a total of 13 individuals from 11 *vinifera* cultivars, nine *sylvestris* accessions and one accession of *V. rotundifolia* (subgenus *Muscadinia*) from the USDA grape germplasm collections in Davis, California (Table 1S). For each sample, genomic DNA was extracted from leaf samples with the Qiagen DNeasy plant kit. Paired-end sequencing libraries were constructed with an insert size of 300 bp according to the Illumina library preparation protocols. Libraries were then sequenced using the Illumina HiSeq 2500 platform with 2 × 150-bp paired reads to a target coverage of 25X. The raw sequencing data have been deposited in the Short Read Archive at NCBI under BioProject ID: PRJNA388292. We also used Illumina raw reads for five other cultivars (1) that were downloaded from the Short Read Archive at NCBI. Altogether we analyzed nine wild accessions and 18 individuals from 14 cultivars, including four Thompson clones and two Zinfandel/Primitivo clones from different geographic regions (Table S1).

Raw read trimming, alignment, and filtering: Paired raw sequencing reads were trimmed using Trimmomatic-0.35 (2) to remove adapter sequences and bases when average quality per base dropped below 20 in 4 bp windows. Reads were discarded when they were <60 bases in length or when they were unpaired after trimming. FastQC (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/) was used to compute the per-base sequence quality for both the raw data and the filtered data. Trimmed reads were mapped to the *V. vinifera* Pinot Noir PN40024 reference genome (12X) (3) with default parameters implemented in bwa-0.7.12 using the BWA-MEM algorithm (4). Local realignment was performed around indels using RealignerTargetCreator and IndelRealigner implemented in GATK v3.5 (5). To account for the occurrence of PCR duplicates introduced during library construction, we used MarkDuplicates in picard-tools 1.119 (https://github.com/broadinstitute/picard) to remove reads with identical external coordinates and insert lengths. Only the read with the highest summed base quality was kept for downstream analyses. To exclude potential errors caused by repetitive DNA sequences, we removed sites with extremely low (< 4 reads per sample) or high (> 4X reads per sample, where X is the mapping depth; Tables S1) read coverage. We also removed multiply mapped reads.

SNP Calling, filtering and annotation: The HaplotypeCaller and GenotypeGVCFs implemented in GATK v3.5 were used for SNP and genotype calling across all samples (5). Four filtering steps were performed to reduce false positives: i) we removed SNPs located in regions not passing all previous filtering criteria; ii) we removed SNPs with more than two alleles in all samples; iii) we assigned genotypes as missing if their quality scores (GQ) were <10; iv) we removed SNPs with more than 75% missing genotypes across all samples.

We determined the functional region (exonic, intronic, and intergenic) in which each mutation occurred using information from the *V. vinifera* genome annotation in Ensembl (version 34). Exonic SNPs were annotated to be synonymous, nonsynonymous and frameshift using the SnpEff version 4.0 (6). Nonsynonymous SNPs were predicted as deleterious or tolerated using the SIFT score (7), as computed in the program SIFT 4G (8). SIFT scores ≤ 0.05 were interpreted as deleterious and SIFT scores > 0.05 were considered to be tolerant. To assess consistency, the PROVEAN score (9) was also computed in the Variant Effect Predictor (VEP, https://github.com/Ensembl/ensembl-vep) with a default cutoff score <2.5 interpreted as deleterious. Results based on PROVEAN are qualitatively identical to those based on SIFT (Fig. S10). The use of the reference genome is expected to decrease the probability that a cultivar variant (as opposed to a wild variant) returns a low PROVEAN or SIFT score (10). We therefore submitted the outgroup instead of the reference allele to prediction programs (11, 12). We calculated the number of variants per individual or per region as equal to 2× homozygous deleterious mutations + heterozygous deleterious mutations (13).

Population Structure: To infer population structure, we used the SAMTools model (14) implemented in the program ANGSD v0.912 (15) to generate a BEAGLE file for the subset of the genome that was determined as being variable, based on a likelihood ratio test ($P < 10^{-6}$) (16). Population structure was then inferred using the program NGSadmix (17), using only sites containing <15% of missing data and a minimal quality score of 20 and a minimal mapping quality of 30. We predefined the number of genetic clusters *K* from 2 to 6, and the maximum iteration of the Expectation Maximization (EM) algorithm was set to 10,000. We also constructed a neighbor joining (NJ) tree based on pairwise relatedness (18) estimated using VCFtools v0.1.14 (https://vcftools.github.io/).

We also performed principal component analyses (PCA) using ngsTools that accounted for sequencing errors and uncertainty in genotype calls (19). The expected covariance matrix across pairs of individuals in both wild samples and cultivated samples was computed based on the genotype posterior probabilities across all filtered sites. Eigenvectors and eigenvalues from the covariance matrix were generated with the R function eigen, and significance levels were determined using the Tracy–Widom test implemented in EIGENSOFT v4.2 (20).

Linkage disequilibrium and genetic diversity: For population genomic analyses, we reduced the sample size to avoid sample replication (Table S1), choosing the individual with the least missing data when we had multiple individuals for a given cultivar. To detect outlier regions of genetic differentiation between wine and table grapes, we used the major lineage of wine or table grapes with pure ancestry in population genetic plots (Figure S1; Table S1).

A total of 1,867,225 SNPs and 1,872,156 SNPs with minor allele frequency > 0.1 were used for the analyses of linkage disequilibrium (LD) and population recombination rate ($\rho = 4N_er$, where N_e is the effective population size and r is the recombination rate per locus) in the wild and the cultivated population, respectively. LD decay along physical distance were measured by the squared correlation coefficients (r^2) between all pairs of SNPs within a physical distance of 300 kbp using PLINK 1.9 (21). The decay of LD against physical distance was estimated using nonlinear regression of pairwise r^2 *vs.* the physical distance between SNPs (22). The population recombination rate ρ were computed using the program LDhat 2.2 (23) with 100,000 burn-in iterations, and 1,000,000 MCMC iterations sampling every 2000 iterations and a block penalty parameter of 5. We calculated the scaled value of ρ in each 100-kbp window with > 1000 SNPs by averaging over all SNPs in that window. Our LD analyses showed decay within 20Kbp in both the wild population and the cultivated population, we therefore use a 20kbp window size in downstream diversity analyses.

To measure genome-wide genetic diversity and allele frequency, we estimated population genetic statistics directly from genotype likelihood without calling genotypes in the software ANGSD v0.912 (15). Only reads with a mapping quality > 30 and bases with a quality score > 20 were considered. We used the −doSaf to calculate the site allele frequency likelihood based on the SAMTools genotype likelihood model at all sites (14), and then used the −realSFS to obtain a maximum likelihood estimate of the unfolded SFS using the Expectation Maximization (EM) algorithm (Kim et al. 2011). We then calculated several population genetic statistics, including the number of segregating sites (*S*), Watterson's θ_w (24), pairwise nucleotide differences within populations (π) and between populations (D_{xy}) (25), Tajima's *D* (26) and Fay and Wu's *H* (Fay and Wu 2000). F_{ST} between wild and cultivated - and between wine and table grapes - were then calculated based on the global SFS from ANGSD. *V. rotundifolia* was used as the outgroup to determine ancestral states.

Demographic history: We employed the multiple sequentially Markovian coalescent (MSMC 2.0) (27) to estimate scaled population sizes (N_e) over historical time for both the cultivated and the wild samples (28). Only sites with uniquely mapped reads and sites with coverage depths between 0.5-fold and 3-fold the mean depth were used in analyses. The remaining genomic regions were masked using the script bamCaller.py in MSMC tools. Prior to the analysis, all segregating sites within each group were phased and imputed using Shapeit v2.12 (29), based on a genetic map (30). A generation time of 3 years and a mutation rate of 2.5×10^{-9} mutations per nucleotide per year (31) were used to convert the scaled times and population sizes into real times and sizes. Analyses of population sizes change were conducted for eight haplotypes of table grapes and wine grapes, respectively (Table S1). Divergence time were estimated between the wild and the cultivated population (eight individuals from each population) as well as between table grapes and wine grapes (four individuals from each group; Table S1). SMC++ (32) was also employed to jointly infer population size histories and split times between the cultivated and wild samples and between wine and table grapes (see Table S1). Only SNPs that passed all the filtering steps were used in this analysis.

Genomic signatures of selection: We found that LD decays primarily within 20 kbp in both the wild and the cultivated populations and thus divided the genome into 23,406 non-overlapping windows of 20 kbp in size to investigate patterns of genomic differentiation and signatures of selection. For a window to be included in the downstream analyses, we required at least 1,000 bases after filtering. Levels of genetic differentiation between species at each site were estimated using the method-of-moments F_{ST} estimators implemented in ngsFST from the ngsTools package (19), which calculates indices of the expected genetic variance between and within species from posterior probabilities of sample allele frequencies, without relying on SNP or genotype calling (33). We then averaged F_{ST} values of all sites within each 20 kbp non-overlapping window. As F_{ST} is confounded by within-population diversity, we also calculated pairwise differences between populations (D_{xy}) to detect genomic islands underlying divergent selection between cultivated samples and wild samples (34). SweeD (35) was used to detect selective sweeps based on the CLR test to detect signatures of artificial selection and natural selection in cultivated samples and wild samples, respectively (36). The XP-CLR test (37) were also employed to compare allele frequency differentiation between populations while using wild samples as a reference to detect selective sweeps in the cultivated samples. The XP-CLR scores were estimated across non-overlapping 200-bp windows that were used to estimate a maximum XP-CLR score across 20-kb segments. The 20-kb segments with the top 0.5% of maximum XP-CLR values were considered significant. The genetic distance between SNPs were estimated by LDhat 2.2 (23) to use as input for XP-CLR.

Gene expression analysis: Raw sequencing data were downloaded from the Short Read Archive (NCBI) under accession numbers SRP049306 for berry samples and SRP041212 for flower samples. The data were trimmed using Trimmomatic v.0.36 (Bolger *et al.*, 2014) with the options: LEADING:3 TRAILING:3 SLIDINGWINDOW:10:20 MINLEN:20. Quality-trimmed reads were mapped onto the predicted transcriptome of *V. vinifera* cv. 'PN40024' (version V1 from http://genomes.cribi.unipd.it/grape/) using the aligner Bowtie2 v.2.2.6 (38) with parameters: -q -end-to-end -sensitive -no-unal -p 20. Finally, sam2counts.py version 0.91 (https://github.com/vsbuffalo/sam2counts) was used to extract mapping counts.

For each dataset (i.e., berries or flowers), read count normalization for genes were performed with DESeq2 (39). This package was also used to process the differential gene expression analysis across types of flowers (i.e. Male vs. Female, Male vs. Hermaphrodite, Female vs. Hermaphrodite), and across berry developmental stages (i.e. End of veraison vs. three other stages; Harvest vs. three other stages). For the flower analyses, the different developmental stages were treated as replicates. To construct hierarchical clustering trees, Pearson's correlation values among genes were calculated using the *cor* function in R software. Prior to calculation, we added 1 to each normalized count value and then $\log_2$-transformed the normalized counts. Correlation values were converted into distances by subtracting the correlation values from 1; a dendrogram was generated using the hclust and heatmap.2 functions from *gplots* R package (40). In total 539 of 26,665 genes were expressed more highly in females than in males and hermaphrodites; the ratio (0.022) was used in a binomial test to test for enrichment in the sex-determination region.

Forward Simulations: Forward in time simulations were carried out using fwdpy11 (https://github.com/molpopgen/fwdpy11), a python package for implementing population genetic models with the fwdpp C++ template library (41). 500 replicate simulations were run for each demographic and mating scheme model. In each replicate, a single population was simulated for 8*N_e generations to burn-in an equilibrium level of genetic variation. Then the simulation was paused, and the population was copied once for each demographic and mating scheme model. Each population copy was then subjected to the appropriate demographic and mating scheme for the final generations. Specific model parameters are described below. This approach allows for the effects of the models to be isolated easily.

Analysis of the SMC++ results (Fig. 2) lead to the inference that the ancestral effective population size of the grape is N_e=4e5 and that *vinifera* underwent an approximately linear population decline to N_e=2e4 over the course of 30,000 years, or *g*=1e4 generations. Forward simulations at these population sizes are computationally intensive and unnecessary to illustrate the important qualitative behaviors. Thus, the parameters were scaled such that the ancestral population size was N_e=4e3 with the final population size for N_e=2e2 over the course of g=100 generations.

Three demographic models were simulated (Figure S8): constant population size, a linear population decline from N_e =4e3 to N_e =2e2 over 100 generations, a discrete bottleneck from N_e =4e3 to N_e =2e2 which occurs instantaneously 100 generations in the past and continues with no recovery. In addition, two mating schemes were simulated: strict outcrossing for the whole simulation, and clonal propagation for the final generations. We assume that clonality began at the time of domestication at 8,000 years ago or g=2,667 generations ago. In scaled terms this means we implement clonality for the final 27 generations of the simulation.

The simulations assumed an infinite sites mutation model and random mating, unless otherwise noted. In this model, we do not model a backwards mutation rate. The mutation and recombination rates per base pair were assumed to be μ per bp=2.5e-9 (31) and ρ per bp=5e-10, which was based on analysis of our data (Figure S2). The population scaled mutation and recombination parameters per base pair are therefore θ bp=4e-3 and ρ bp=8e-4. A total genomic length of 1Mb was modeled by setting θ tot=4000 and ρ tot=800. This 1Mb contiguous recombining region was subject to both neutral and unconditionally deleterious mutation assuming that 11/12 (91.7%) of all newly arising mutations are neutral and the remaining 1/12 are deleterious (12). Deleterious mutations affect fitness according to the standard model where the fitness effect of each locus is: *w*= 1, 1+hs, 1+2s, and the fitness of an individual is the product of the effects at each locus. The values of 's' are drawn a negative gamma distribution with mean -0.05 and shape 0.3 (12, 42). Pure additive and recessive selection are modeled by setting h=1 and h=0 respectively (note that h=1 is perfect co-dominance, because homozygotes have fitness of 1+2s). Genetic load is calculated as 1-$\bar{w}$, where $\bar{w}$ is the average population fitness.

SUPPLEMENTAL TEXT CITATIONS

1. Velasco R *et al*. (2007) A high quality draft consensus sequence of the genome of a heterozygous grapevine variety. *PLoS One* 2(12):e1326.
2. Bolger AM, Lohse M, Usadel B (2014) Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics* 30(15):2114–2120.
3. Jaillon O *et al*. (2007) The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla. *Nature* 449(7161):463–467.
4. Li H (2014) Toward better understanding of artifacts in variant calling from high-coverage samples. *Bioinformatics* 30(20):2843–2851.
5. DePristo MA *et al*. (2011) A framework for variation discovery and genotyping using next-generation DNA sequencing data. *Nat Genet* 43(5):491–498.
6. Cingolani P *et al*. (2012) A program for annotating and predicting the effects of single nucleotide polymorphisms, SnpEff: SNPs in the genome of Drosophila melanogaster strain w1118; iso-2; iso-3. *Fly (Austin)* 6(2):80–92.
7. Kumar P, Henikoff S, Ng PC (2009) Predicting the effects of coding non-synonymous variants on protein function using the SIFT algorithm. *Nat Protoc* 4(7):1073–1081.
8. Vaser R, Adusumalli S, Leng SN, Sikic M, Ng PC (2016) SIFT missense predictions for genomes. *Nat Protoc* 11(1):1–9.
9. Choi Y, Sims GE, Murphy S, Miller JR, Chan AP (2012) Predicting the functional effect of amino acid substitutions and indels. *PLoS One* 7(10):e46688.
10. Lohmueller KE *et al*. (2008) Proportionally more deleterious genetic variation in European than in African populations. *Nature* 451(7181):994–997.
11. Kono TJ *et al*. (2016) The Role of Deleterious Substitutions in Crop Genomes. *Mol Biol Evol*
12. Liu Q, Zhou Y, Morrell PL, Gaut BS (2017) Deleterious Variants in Asian Rice and the Potential Cost of Domestication. *Mol Biol Evol* 34(4):908–924.
13. Henn BM *et al*. (2016) Distance from sub-Saharan Africa predicts mutational load in diverse human genomes. *Proc Natl Acad Sci U S A* 113(4):E440–9.
14. Li H *et al*. (2009) The Sequence Alignment/Map format and SAMtools. *Bioinformatics* 25(16):2078–2079.
15. Korneliussen TS, Albrechtsen A, Nielsen R (2014) ANGSD: Analysis of Next Generation Sequencing Data. *BMC Bioinformatics* 15:356.
16. Kim SY *et al*. (2011) Estimation of allele frequency and association mapping using next-generation sequencing data. *BMC Bioinformatics* 12:231.
17. Skotte L, Korneliussen TS, Albrechtsen A (2013) Estimating individual admixture proportions from next generation sequencing data. *Genetics* 195(3):693–702.
18. Yang J *et al*. (2010) Common SNPs explain a large proportion of the heritability for human height. *Nat Genet* 42(7):565–569.
19. Fumagalli M, Vieira FG, Linderoth T, Nielsen R (2014) ngsTools: methods for population genetics analyses from next-generation sequencing data. *Bioinformatics* 30(10):1486–1487.
20. Patterson N, Price AL, Reich D (2006) Population structure and eigenanalysis. *PLoS Genet*

2(12):e190.

21. Purcell S *et al.* (2007) PLINK: a tool set for whole-genome association and population-based linkage analyses. *Am J Hum Genet* 81(3):559–575.
22. Hill WG, Robertson A (1968) Linkage disequilibrium in finite populations. *Theor Appl Genet* 38:226–231.
23. McVean GA *et al.* (2004) The fine-scale structure of recombination rate variation in the human genome. *Science* 304(5670):581–584.
24. Watterson GA (1975) On the number of segregating sites in genetical models without recombination. *Theor Popul Biol* 7(2):256–276.
25. Nei M (1987) *Molecular Evolutionary Genetics* (Columbia University Press, New York, NY).
26. Tajima F (1989) Statistical method for testing the neutral mutation hypothesis by DNA polymorphism. *Genetics* 123:585–595.
27. Li H, Durbin R (2011) Inference of human population history from individual whole-genome sequences. *Nature* 475(7357):493–496.
28. Schiffels S, Durbin R (2014) Inferring human population size and separation history from multiple genome sequences. *Nat Genet* 46(8):919–925.
29. Delaneau O, Zagury JF, Marchini J (2013) Improved whole-chromosome phasing for disease and population genetic studies. *Nat Methods* 10(1):5–6.
30. Hyma KE *et al.* (2015) Heterozygous Mapping Strategy (HetMappS) for High Resolution Genotyping-By-Sequencing Markers: A Case Study in Grapevine. *PLoS One* 10(8):e0134880.
31. Koch MA, Haubold B, Mitchell-Olds T (2000) Comparative evolutionary analysis of chalcone synthase and alcohol dehydrogenase loci in Arabidopsis, Arabis, and related genera (Brassicaceae). *Mol Biol Evol* 17(10):1483–98.
32. Terhorst J, Kamm JA, Song YS (2017) Robust and scalable inference of population history from hundreds of unphased whole genomes. *Nat Genet* 49(2):303–309.
33. Fumagalli M *et al.* (2013) Quantifying population genetic differentiation from next-generation sequencing data. *Genetics* 195(3):979–992.
34. Cruickshank TE, Hahn MW (2014) Reanalysis suggests that genomic islands of speciation are due to reduced diversity, not reduced gene flow. *Mol Ecol* 23(13):3133–3157.
35. Pavlidis P, Zivkovic D, Stamatakis A, Alachiotis N (2013) SweeD: likelihood-based detection of selective sweeps in thousands of genomes. *Mol Biol Evol* 30(9):2224–2234.
36. Nielsen R *et al.* (2005) Genomic scans for selective sweeps using SNP data. *Genome Res* 15(11):1566–1575.
37. Chen H, Patterson N, Reich D (2010) Population differentiation as a test for selective sweeps. *Genome Res* 20(3):393–402.
38. Langmead B, Salzberg SL (2012) Fast gapped-read alignment with Bowtie 2. *Nat Methods* 9(4):357–359.
39. Love MI, Huber W, Anders S (2014) Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. *Genome Biol* 15(12):550.
40. Warnes GR *et al.* (2009) gplots: Various R programming tools for plotting data. *R package version* 2:4.
41. Thornton KR (2014) A C++ template library for efficient forward-time population genetic simulation of large populations. *Genetics* 198(1):157–166.
42. Arunkumar R, Ness RW, Wright SI, Barrett SC (2015) The evolution of selfing is accompanied by reduced efficacy of selection and purging of deleterious mutations. *Genetics* 199(3):817–829.

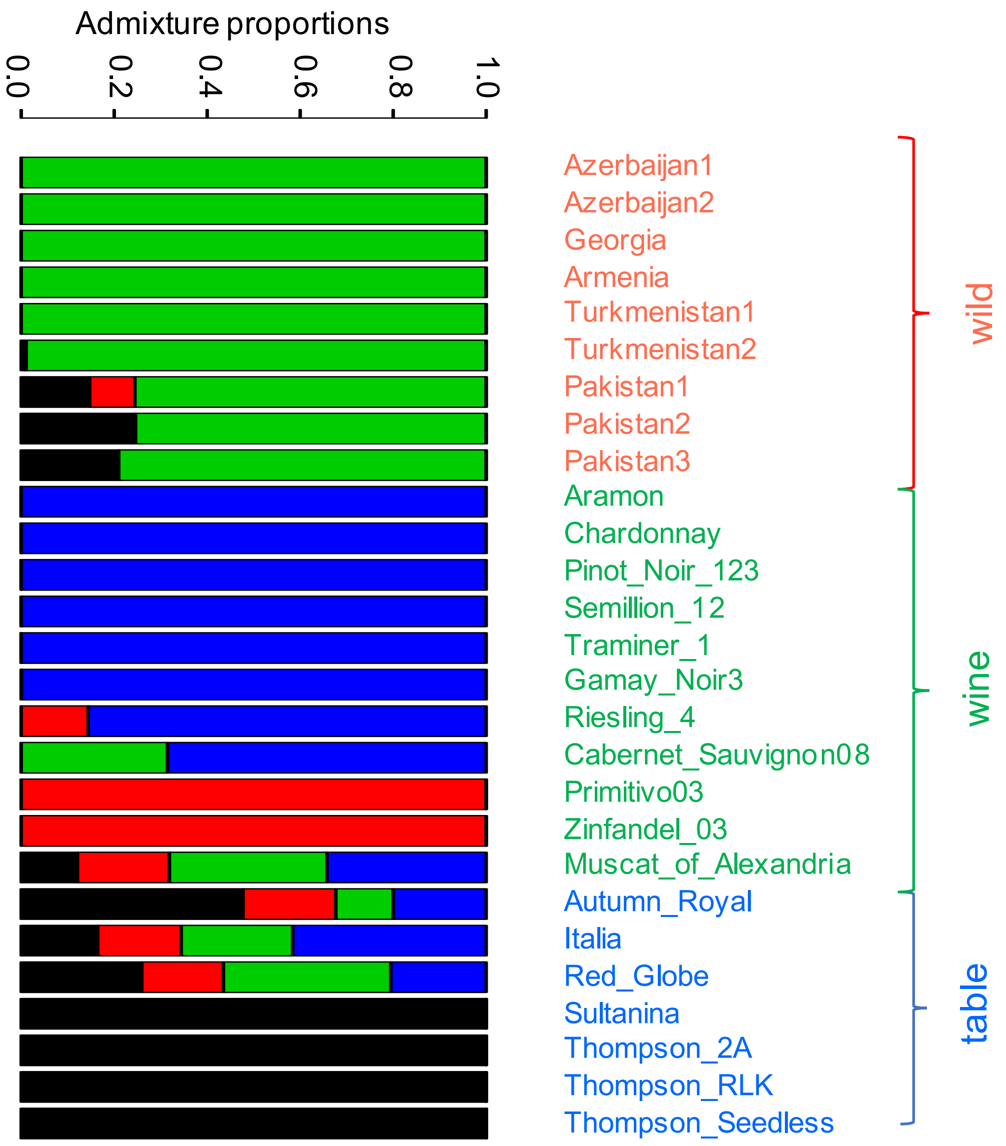


Figure S1. Population structure of cultivars and wild samples. Population genetic structure of wild samples and cultivars inferred using NGSadmix with number of ancestral clusters $K = 4$. The x -axis quantifies subgroup membership, and the y -axis shows the sample ID for each individual grouped into wild, wine, and table grapes.

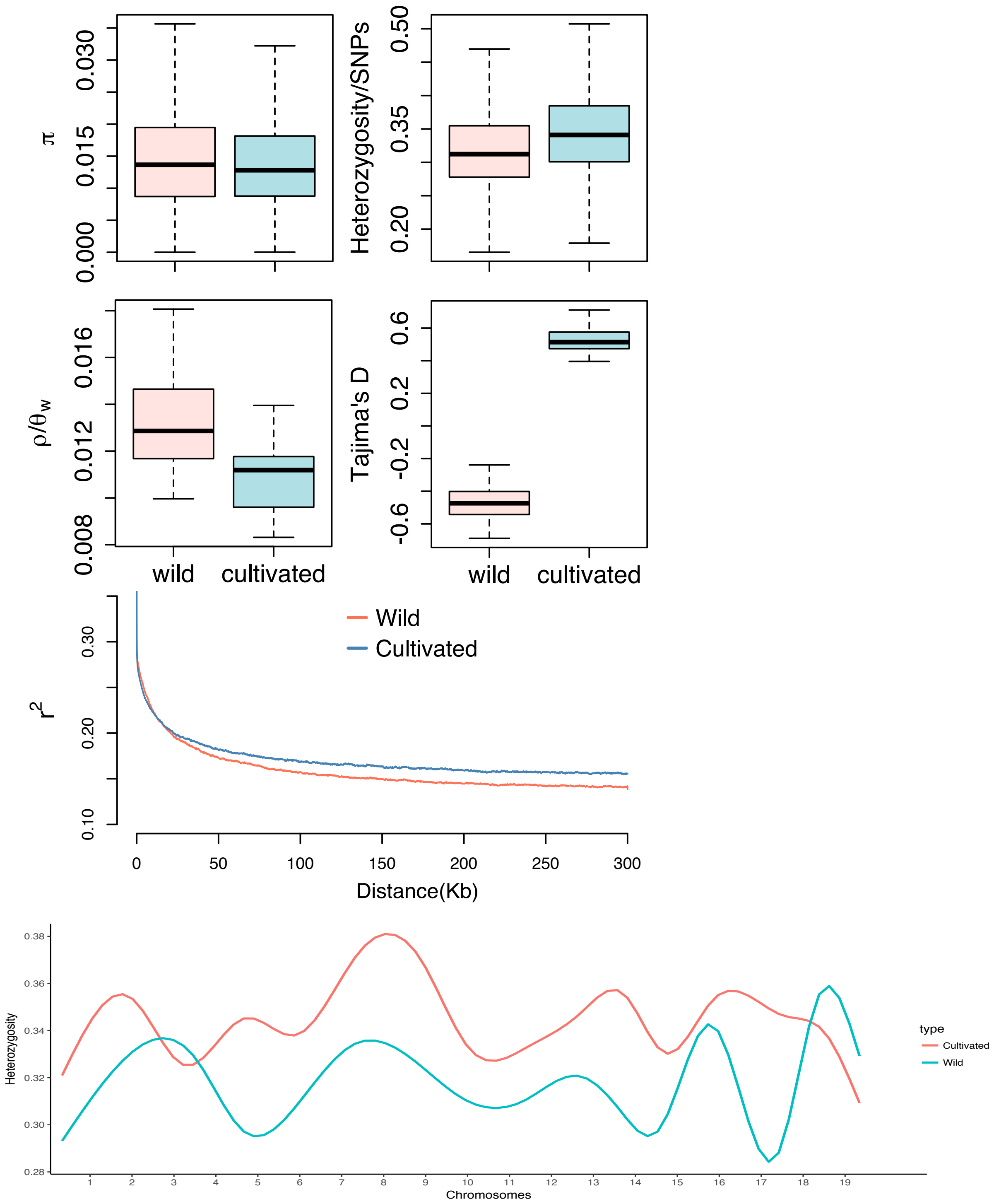
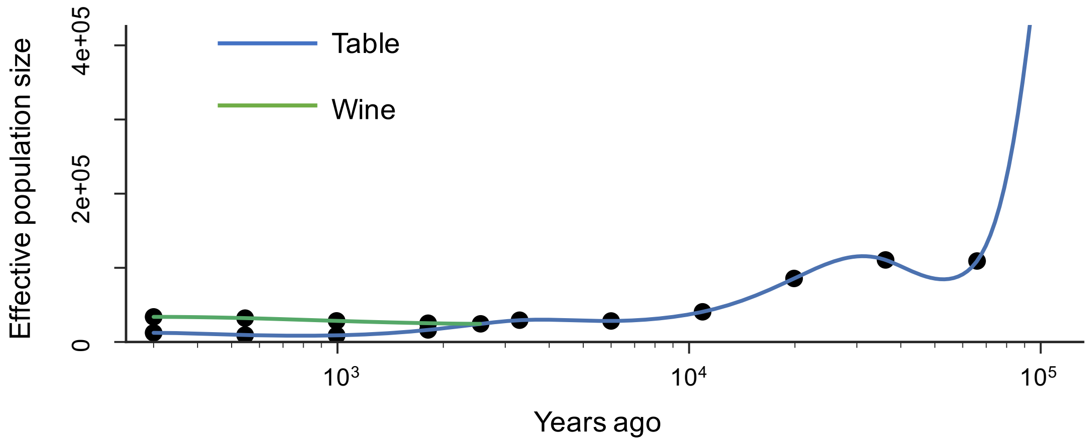


Figure S2. Comparison of levels of nucleotide diversity, recombination, LD and heterozygosity between the wild samples and the cultivars. Top box plots illustrate pairwise differences (π), Heterozygosity/SNP, the ratio of population recombination rate to population mutation rate (ρ/θ_w), Tajima's *D* between *vinifera* and *sylvestris*. The middle graph illustrates LD decay as measured by the squared correlation coefficients (r^2) between all pairs of SNPs. The bottom graphs illustrate heterozygosity for wild and cultivated samples along chromosomes.



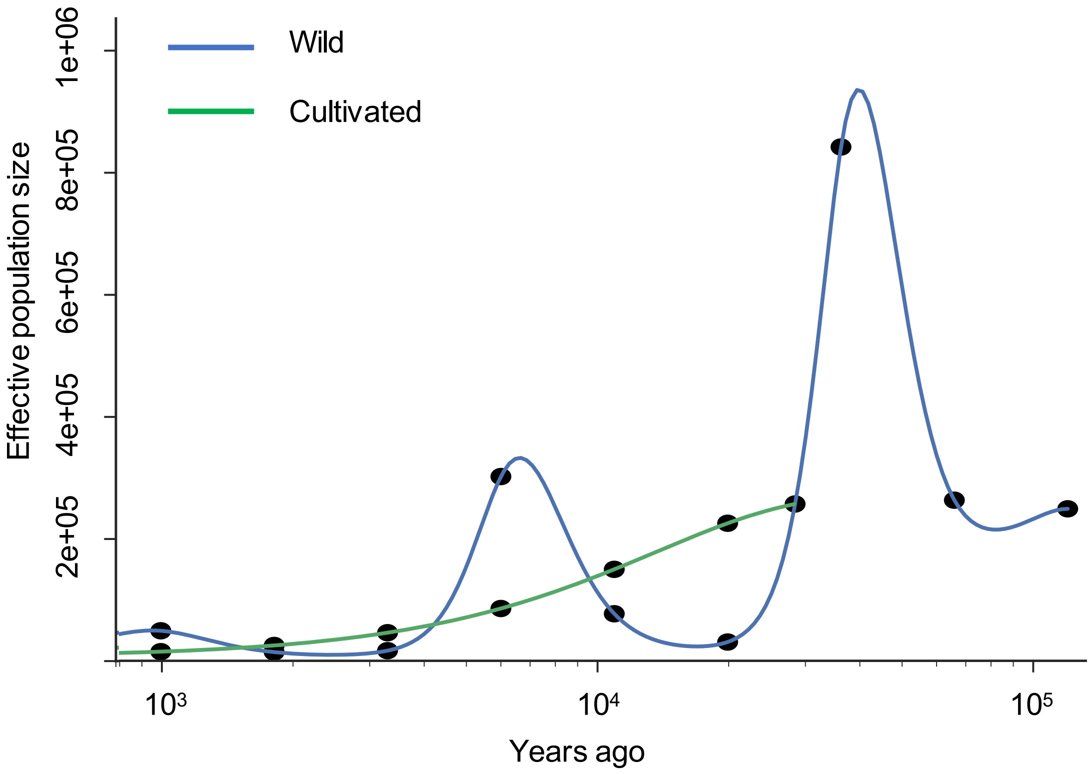


Figure S3. Results of the SMC++ analyses between wine and table grapes dated the divergence at ~ 2.6 Kya (upper), and between wild samples and cultivars with the selective sweep regions masked in both taxa (lower). The masked sweep regions were based on CLR analyses.

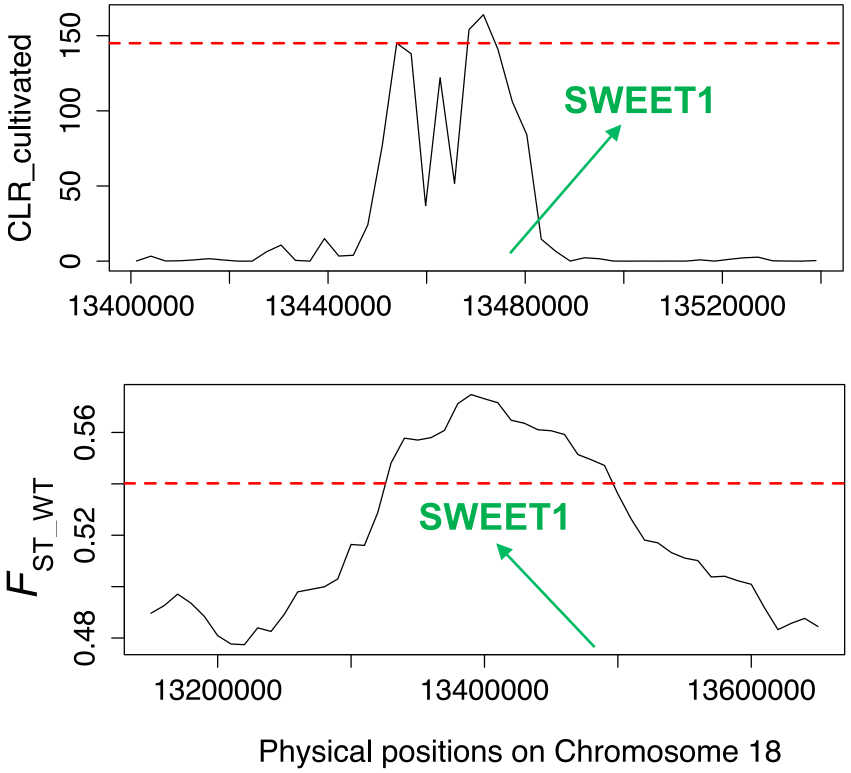


Figure S4. The *SWEET1* gene (a bidirectional sugar transporter) is located within an inferred sweep region based on CLR analysis of *vinifera* (top) and is also evident in an F_{ST} analysis between wine and table grapes (bottom).

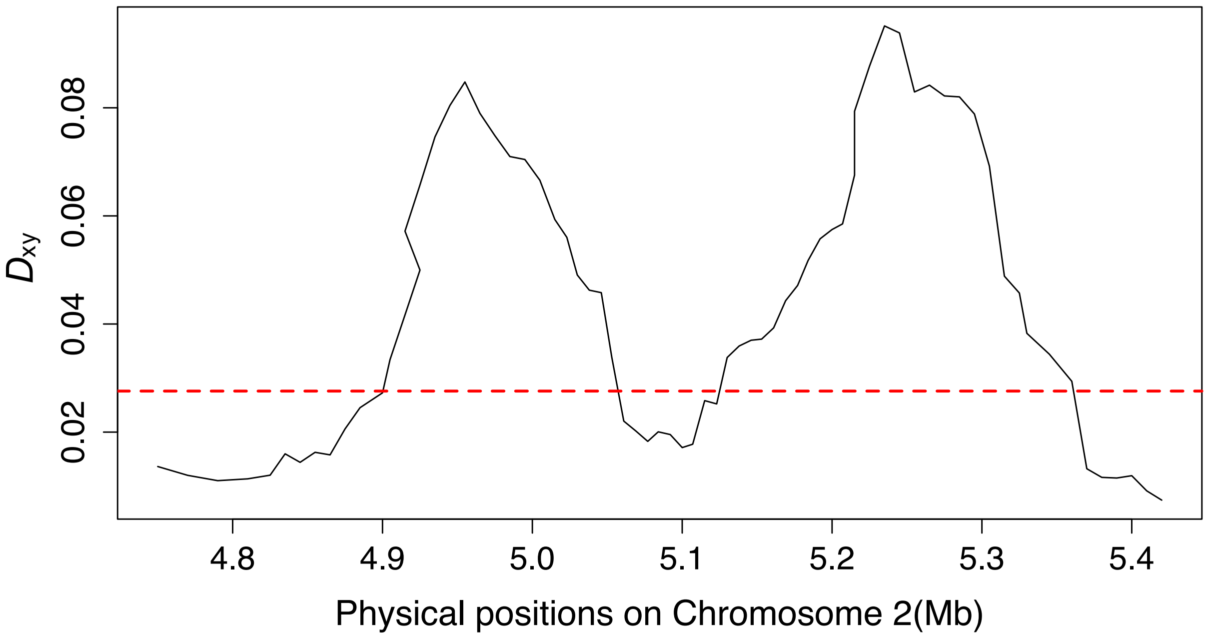


Figure S5. Pairwise difference (D_{xy}) between *vinifera* and *sylvestris* identified two peaks in the sex determination region on Chromosome 2.

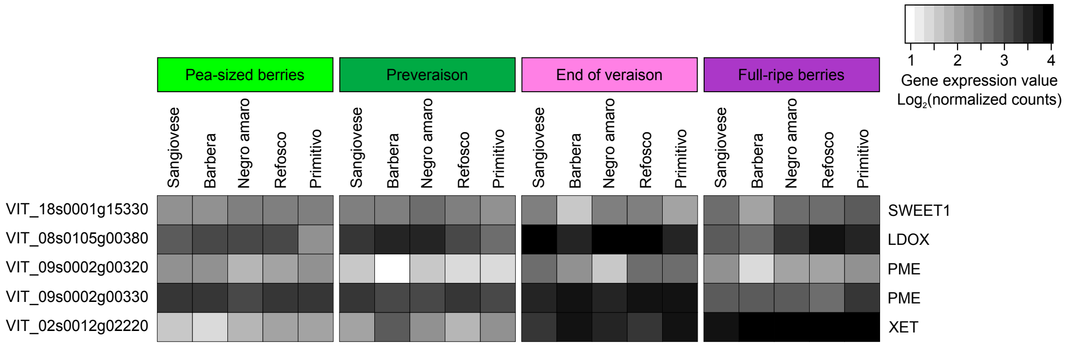


Figure S6. Heat map of selected *vinifera* candidate-selected genes during berry development in five red cultivars (Palumbo *et al*., 2014). Heat map depicts the $\log_2$-transformed of the normalized read counts (average of the three biological replicates) of the sugar transporter gene *SWEET1*, a leucoanthocyanidin dioxygenase (*LDOX*) gene, two pectinesterase (*PME*) genes and a xyloglucan endotransglucosylase/hydrolase (*XET*) gene.

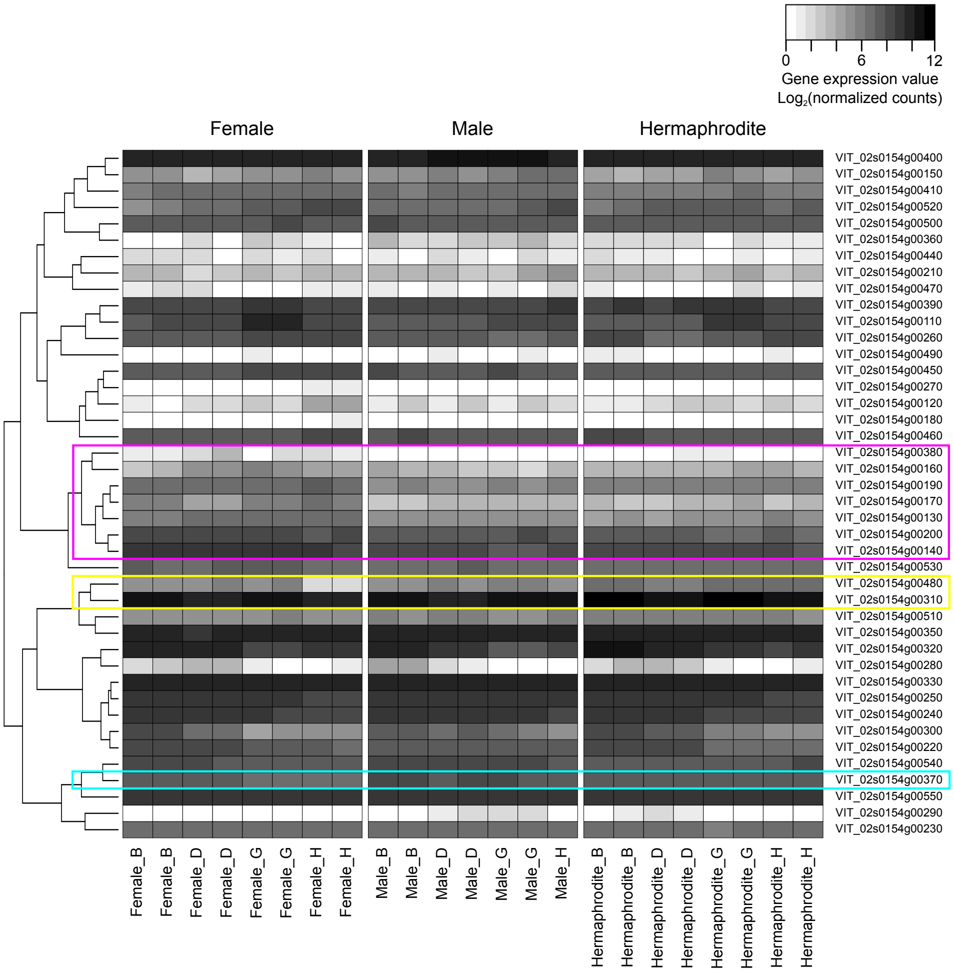


Figure S7. Hierarchical clustering heat map of the sex determination region genes in female, male and hermaphrodite flowers (Ramos *et al*., 2014). Pink, blue and yellow frames shows genes overexpressed in female, male and hermaphrodite flowers respectively.

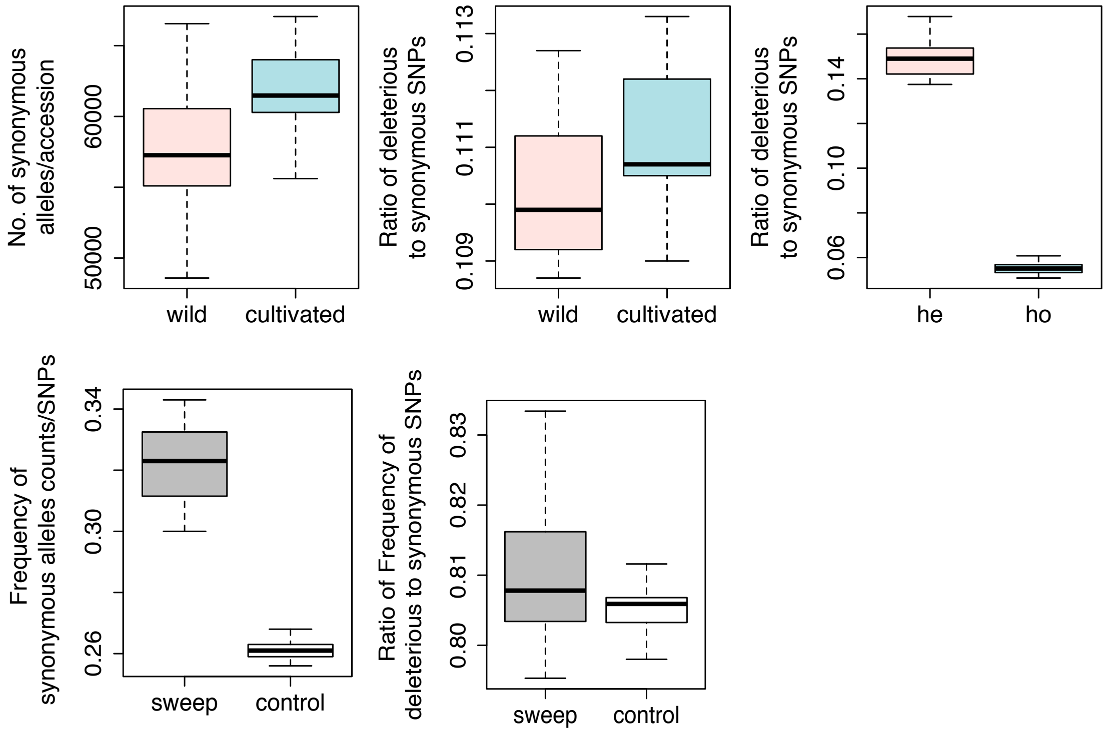


Figure S8. Number and Frequency of deleterious alleles between wild and cultivated grapes, and between sweep regions and control regions in *vinifera*, based on SIFT predictions.

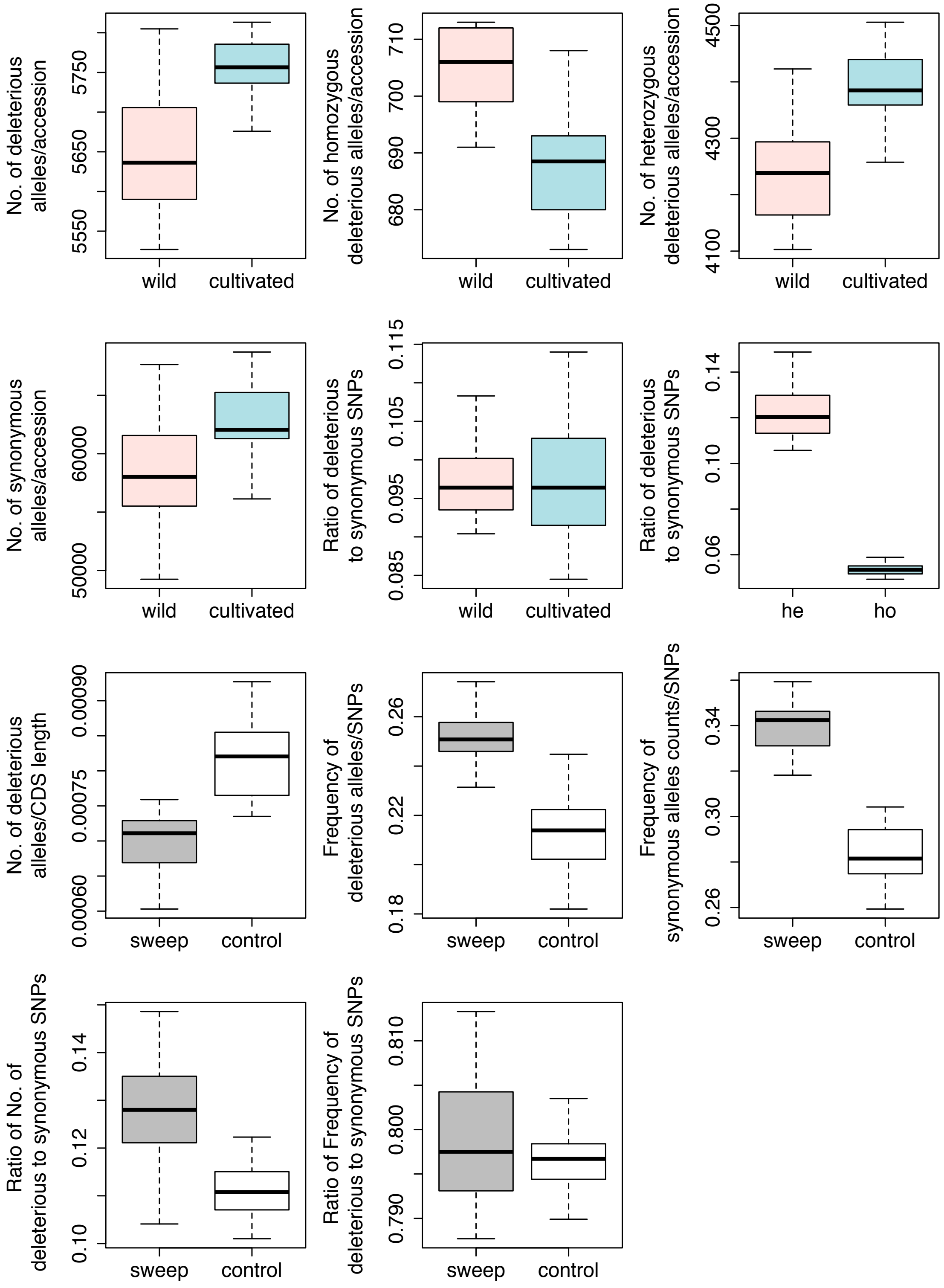


Figure S9. Number and Frequency of deleterious alleles between wild and cultivated grapes, and between sweep regions and regions in *vinifera* using the PROVEAN method.

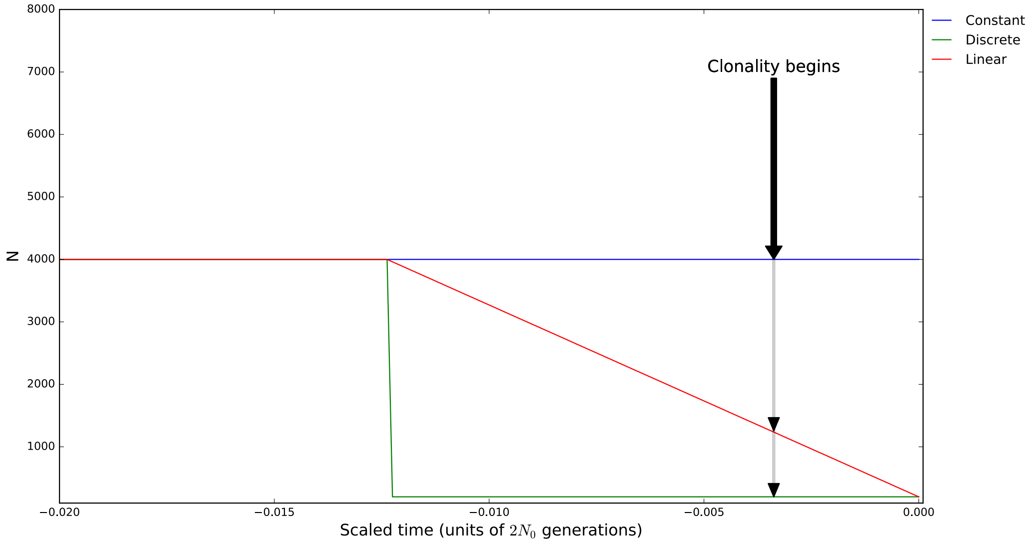


Figure S10. The model used in forward simulations over time under three demographic scenarios and two mating systems. Demographic shifts were scaled to ~30,000 years and clonality to ~8,000 years, roughly the expected time of domestication.

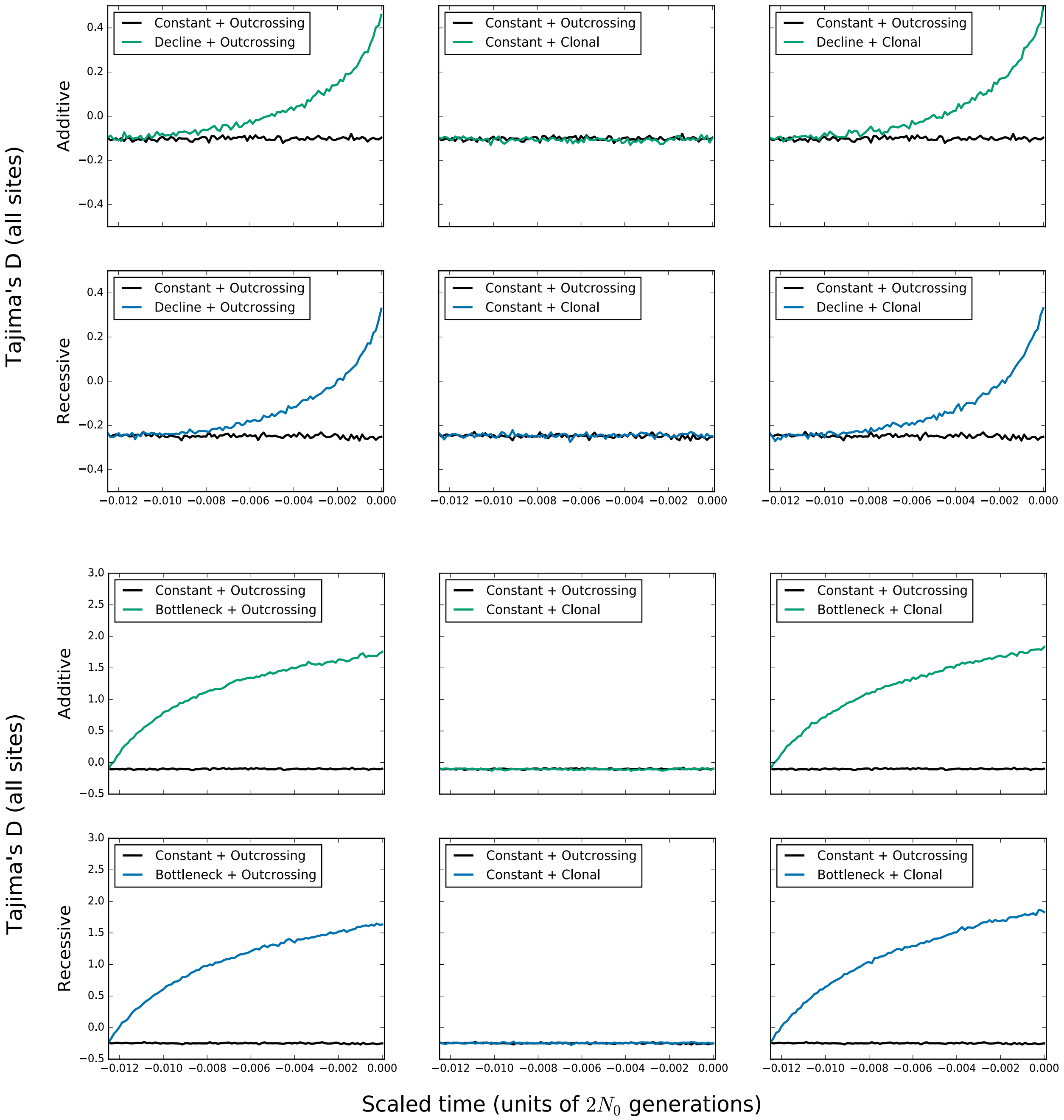


Figure S11. Tajima's *D* statistic over time for models with a linear population decline and/or clonal propagation (upper six plots), and a discrete population bottleneck and/or clonal propagation (lower six plots). Tajima's *D* was calculated using all segregating sites in a sample of 100 diploid individuals. Data are displayed as the mean plus or minus the standard error over 500 replicate simulations, based on a total genomic length of 10kb. The upper row shows the results for additive selection, while the lower row shows the results for recessive selection. In each panel, the model with a constant population size and outcrossing is shown for reference.

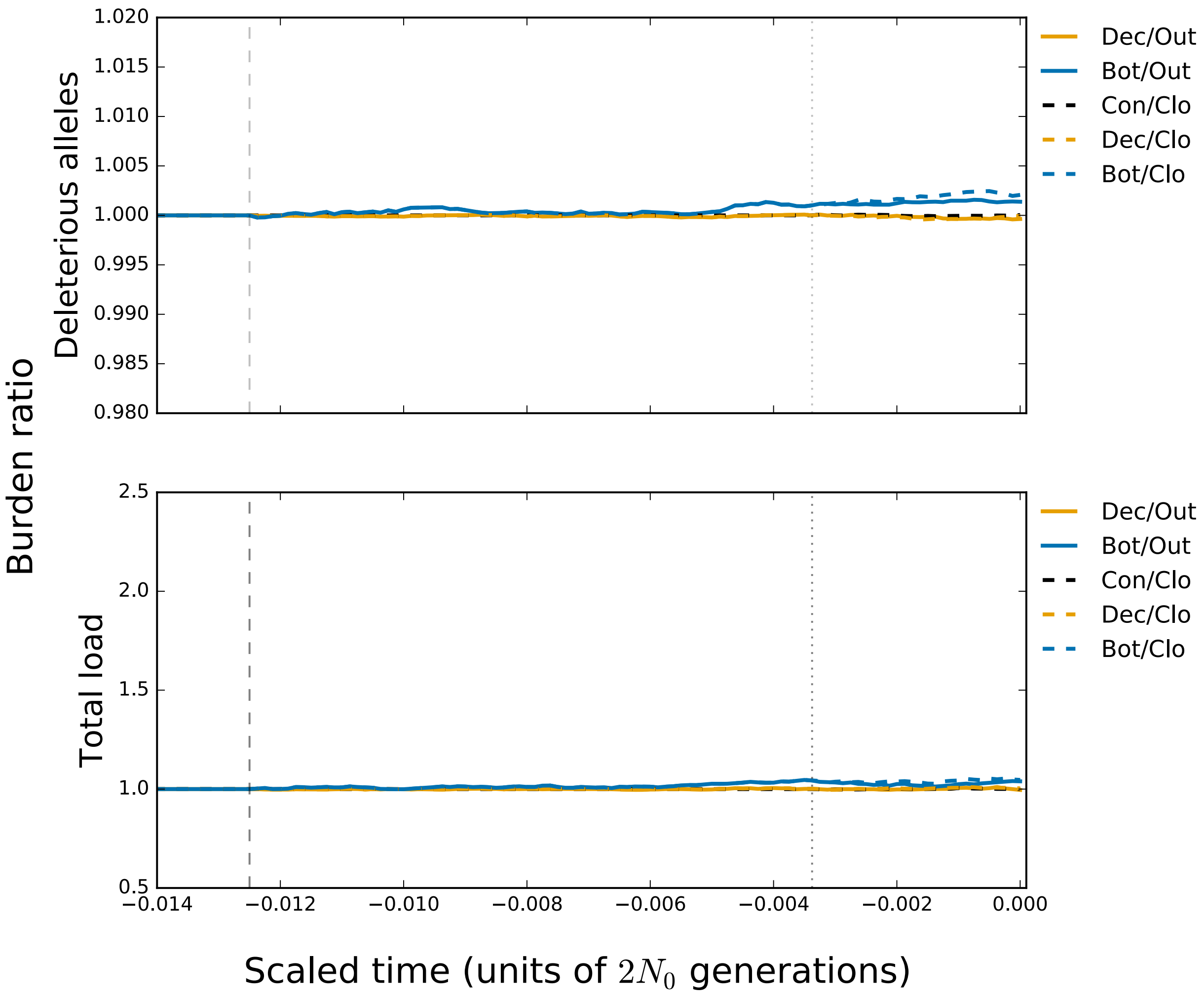


Figure S12. Forward simulations under a model of additive mutations (dominant coefficient *h* = 0.5) for three demographic scenarios and two mating systems. The top graph represents the average number of deleterious alleles per accession relative to an outcrossing population of constant size. The bottom graph represents the total load relative to an outcrossing population of constant size. The dashed lines represent the time of demographic shift, ~30k years ago, and the onset of clonal propagation during domestication ~8k years ago. Data are displayed as the mean plus or minus the standard error over 500 replicate simulations. Abbreviations for demographic models are: Con = constant population size; Dec = declining population size; Bot = bottleneck. Abbreviations for mating schemes are: Out = outcrossing; Clo = clonal propagation.

SUPPLEMENTARY TABLES:

Table S1 Summary statistics of sequenced samples

Sample	Accession No.	%unique mapped	Mapping depth	%ref covered	Data from	**Analyses[1]**
V. rotundifolia	DVIT_2248	62.84	16.46	0.69	Our effort	Outgroup
V. vinifera ssp. *sylvestris*						
Azerbaijan1	DVIT_3599	90.21	14.7	0.88	Our effort	1,2,3,4
Azerbaijan2	DVIT_3608	89.38	13.38	0.86	Our effort	1,2,4
Georgia	DVIT_3350	91.42	10.89	0.89	Our effort	1,2,3,4
Armenia	DVIT_3351	88.03	9.75	0.86	Our effort	1,2,3,4
Turkmenistan1	DVIT_2447	90.41	10.02	0.88	Our effort	1,2
Turkmenistan2	DVIT_2445	91.3	10.83	0.9	Our effort	1,2,4
Pakistan1	DVIT_2261	91.64	13.06	0.92	Our effort	1,2,4
Pakistan2	DVIT_2266	91.56	15.14	0.93	Our effort	1,2,3,4
Pakistan3	DVIT_2269	90.72	13.67	0.93	Our effort	1,2,4
V. vinifera ssp. *vinifera*						
Aramon	DVIT_633	91.54	14.02	0.93	Our effort	1,2,3,4,5
Chardonnay_04	DVIT_1332	91.29	48.94	0.98	Our effort	1,2,3,4,5
Gamay_Noir3	DVIT_8071	91.76	10.04	0.9	Our effort	1,2,5
Pinot_Noir_123	DVIT_914	91.89	13.3	0.94	Our effort	1,2,5
Primitivo_03	PI_325796	89.16	20.57	0.95	Our effort	1,2,3,4
Cabernet_Sauvignon08	DVIT_677	91.61	10.67	0.9	Our effort	1,2,3,4
Riesling_4	DVIT_8143	91.51	11.51	0.91	Our effort	1,2,3,4
Semillion_12	DVIT_1338	91.28	20.97	0.9	Our effort	1,2,5
Traminer_1	DVIT_8186	91.45	18.97	0.87	Our effort	1,2,5
Zinfandel_03	DVIT_1343	91.51	33.53	0.96	Our effort	1,2
Muscat_of_Alexandria	DVIT_8114	91.64	11.82	0.91	Our effort	1,2
Autumn_Royal		88.59	12.92	0.81	Cardone et al. 2016	1,2,3,4
Italia		88.44	11.61	0.85	Cardone et al. 2016	1,2,3,4
Red_Globe		89.2	11.66	0.84	Cardone et al. 2016	1,2,3,4
Sultanina		91.14	62.34	0.97	Genova et al. 2014	1,2,3,4,5
Thompson_2A	DVIT_535	91.73	12.72	0.91	Our effort	1,5
Thompson_RLK	DVIT_8178	91.33	10.82	0.89	Our effort	1,5
Thompson_Seedless		90.48	11.69	0.85	Cardone et al. 2016	1,5

Analyses: 1, population structure; 2, sweep mapping; 3, MSMC; 4, SMC++; 5, F_{ST} between table and wine grapes

Table S2 Lists of genes identified as potentially selected, based on CLR, F_{ST}, Dxy and XP-CLR analyses.

CLR_ *vinifera*		
Gene stable ID	**Functional annotation**	**Arabidopsis homolog**
VIT_01s0011g06260	Anthranilate synthase beta subunit	AT1G25220
VIT_01s0011g06270	Hydroxyproline-rich glycoprotein	AT1G14710
VIT_01s0011g06280	Oxidoreductase	AT1G68080
VIT_01s0011g06290	Purple acid phosphatase 3 ATPAP3/PAP3	AT1G14700
VIT_01s0011g06300	Annexin 5 (ANN5)	AT1G68090
VIT_01s0011g06310	Inositol polyphosphate related phosphatase	AT2G01900
VIT_02s0012g00820	Unknown	-
VIT_02s0012g00830	Expansin-like B1	AT4G17030
VIT_02s0012g00840	Pentatricopeptide (PPR) repeat-containing protein	AT1G08070
VIT_02s0012g00850	Splicing factor PWI domain-containing protein	AT1G31870
VIT_02s0012g00860	No hit	-
VIT_02s0012g00870	RNA-binding protein 10	AT3G54230
VIT_02s0012g01950	Photosystem II protein D1	-
VIT_02s0012g01960	Transcription factor jumonji (jmj)	AT5G46910
VIT_02s0012g02190	Cellulose synthase CSLD2	AT5G16910
VIT_02s0012g02200	No hit	-
VIT_02s0012g02210	No hit	-
VIT_02s0012g02220	Xyloglucan endotransglucosylase/hydrolase 30	AT1G32170
VIT_02s0109g00280	No hit	-
VIT_02s0109g00290	CYP76C6	-
VIT_02s0109g00300	CYP76B1	AT3G61040
VIT_02s0241g00120	Receptor protein kinase	AT4G22730
VIT_02s0241g00130	No hit	-
VIT_02s0241g00140	Calmodulin (A)	AT1G12310
VIT_02s0241g00150	No hit	-
VIT_02s0241g00160	Esterase/lipase/thioesterase family	AT4G12230
VIT_02s0241g00170	Zinc finger (C2H2 type) family	AT4G12240
VIT_03s0017g00760	E3 ubiquitin-protein ligase HUWE1	-
VIT_03s0017g00770	Diacylglycerol kinase 2	-
VIT_03s0097g00380	Monofunctional aspartokinase	AT5G13280
VIT_03s0097g00390	Unknown protein	AT1G33780
VIT_03s0110g00180	No hit	-
VIT_03s0110g00190	Cytochrome oxidase subunit 1	ATMG01360
VIT_03s0110g00200	Apocytochrome b	ATMG00220

VIT_04s0008g03610	Xylan synthase	AT1G27600
VIT_04s0008g03620	Catalytic	AT5G11560
VIT_04s0008g03630	Binding	AT5G11550
VIT_04s0008g03640	FAD-binding domain-containing protein	AT5G11540
VIT_04s0008g03650	Embryonic flower 1	-
VIT_04s0008g03660	Embryonic flower 1	AT5G11530
VIT_04s0008g03670	Tesmin/TSO1-like CXC domain-containing	AT4G29000
VIT_04s0008g06060	Unknown	-
VIT_04s0008g06070	Aberrant root formation protein 4 ALF4	AT5G11030
VIT_04s0008g06080	Unknown protein	AT5G11040
VIT_04s0008g06090	Pentatricopeptide (PPR) repeat	AT1G08070
VIT_04s0008g06130	KNAT2 (knotted1-like homeobox gene 3)	AT5G25220
VIT_04s0008g06140	No hit	-
VIT_04s0008g06150	No hit	-
VIT_04s0008g06160	Neurochondrin family protein	AT4G32050
VIT_04s0008g06170	Unknown protein	AT5G25265
VIT_04s0008g06180	Histone-lysine N-methyltransferase ATX1	AT2G31650
VIT_04s0008g06190	Polyprotein	-
VIT_08s0032g00290	RNA-binding region RNP-1	AT5G32450
VIT_08s0032g00300	Annexin A3	AT5G12380
VIT_08s0032g00310	Ubiquitin-conjugating enzyme E2 A	AT2G02760
VIT_08s0032g00320	Pigment defective 318 (PDE318)	AT1G80770
VIT_08s0032g00330	Pigment defective 318 (PDE318)	AT1G80770
VIT_08s0032g00340	No hit	-
VIT_08s0032g00350	No hit	-
VIT_08s0032g00360	N-6 Adenine-specific DNA methylase	AT3G58470
VIT_08s0032g00370	No hit	-
VIT_08s0032g00380	Myosin-like protein XIC	AT1G08730
VIT_08s0032g00390	Myosin-like protein	AT1G17580
VIT_08s0032g00400	Unknown	-
VIT_08s0032g00410	Myosin-like protein XIK	AT5G20490
VIT_08s0032g00420	Exostosin	AT4G38040
VIT_08s0032g00440	Syntaxin 1B/2/3/4	AT5G08080
VIT_08s0032g00450	No hit	-
VIT_08s0032g01110	Axial regulator YABBY2	AT1G08465
VIT_08s0032g01120	Pentatricopeptide repeat-containing protein	-
VIT_08s0032g01130	Caffeic acid methyltransferase	AT5G54160
VIT_08s0032g01140	Unknown protein	AT5G16280
VIT_08s0105g00260	Digalactosyldiacylglycerol synthase 1	AT3G11670
VIT_08s0105g00270	NC domain-containing protein	AT5G06370

VIT_08s0105g00280	Ribosomal protein S8e	AT5G06360
VIT_08s0105g00290	Zinc finger (C3HC4-type ring finger)	AT5G01450
VIT_08s0105g00300	Phospholipase C	AT3G08510
VIT_08s0105g00310	Rhodanese domain-containing protein	AT3G08920
VIT_08s0105g00330	Enhanced silencing phenotype 4 ESP4 symplekin	AT5G01400
VIT_08s0105g00340	NLI interacting factor (NIF)	AT3G55960
VIT_08s0105g00350	DnaJ homolog, subfamily B, member 4	AT3G08910
VIT_08s0105g00360	PHD finger protein alfin	AT5G05610
VIT_08s0105g00370	Myb family	AT2G01060
VIT_08s0105g00380	Leucoanthocyanidin dioxygenase	AT3G11180
VIT_08s0105g00390	Calcium-dependent protein kinase 13 CPK13	AT3G51850
VIT_08s0105g00400	GT-1-like transcription factor	AT2G38250
VIT_08s0105g00410	Transposase, IS4	AT5G41980
VIT_08s0105g00420	Unknown	-
VIT_08s0105g00430	Omega-3 fatty acid desaturase, chloroplast precursor	AT5G05580
VIT_08s0105g00440	Selenoprotein	AT5G58640
VIT_08s0105g00450	Transducin protein	AT5G05570
VIT_08s0105g00460	Acyl-CoA oxidase (ACX4)	AT3G51840
VIT_09s0002g00230	Pentatricopeptide (PPR) repeat-containing protein	AT3G18020
VIT_09s0002g00260	Unknown protein	-
VIT_09s0002g00280	Ubiquitin-conjugating enzyme E2 J2	AT5G50430
VIT_09s0002g00300	APUM23 (Arabidopsis PUMILIO 23)	AT1G72320
VIT_09s0002g00310	ATP synthase CF0 A subunit	AT5G60390
VIT_09s0002g00320	Pectinesterase PME3	AT3G14310
VIT_09s0002g00330	Pectinesterase PME1	AT1G53840
VIT_10s0003g04520	No hit	-
VIT_10s0003g04530	Cation: chloride symporter	AT1G30450
VIT_10s0042g00010	Strictosidine synthase	-
VIT_10s0042g00020	Strictosidine synthase	AT3G57030
VIT_10s0042g00720	ATP-dependent RNA helicase	-
VIT_10s0042g00760	No hit	-
VIT_10s0042g00770	Leucine-rich repeat receptor-like protein kinase 1	AT4G08850
VIT_10s0042g00780	Gag-pol polyprotein	-
VIT_10s0042g00790	Unknown	-
VIT_10s0042g00800	Proteasome 26S regulatory subunit (RPN2)	AT2G32730
VIT_10s0042g00950	Succinyl-CoA ligase alpha 1 subunit	AT5G23250
VIT_10s0042g00960	DNAJ heat shock N-terminal domain-containing protein	AT5G23240
VIT_10s0092g00470	SHR5-receptor-like kinase	AT1G56130
VIT_10s0092g00480	CYP71D10p	AT3G26330
VIT_10s0092g00490	CYP71A12	-

VIT_10s0092g00500	CYP71D10	AT5G25120
VIT_10s0092g00510	CYP71D10p	AT3G26310
VIT_10s0092g00520	Leucine-rich repeat family	-
VIT_10s0092g00560	Transducin protein	AT2G16405
VIT_10s0092g00570	Leucine-rich repeat family	AT1G56140
VIT_10s0092g00580	No hit	-
VIT_10s0092g00590	Leucine-rich repeat family	AT1G56140
VIT_10s0092g00690	Cysteine-rich receptor-like protein kinase 8	AT4G23160
VIT_10s0092g00780	F-type H+-transporting ATPase alpha chain	ATMG01190
VIT_10s0092g00790	Ribosomal protein S19	-
VIT_11s0016g01710	Myosin-like protein XIK	AT5G20490
VIT_11s0016g01720	Threonine synthase	AT4G29840
VIT_11s0016g01730	VIP3 (vernalization independence 3)	AT4G29830
VIT_11s0016g01740	Zinc finger (C2H2 type) family	AT2G19385
VIT_11s0016g01750	Unknown protein	AT4G26060
VIT_11s0016g01760	Cleavage and polyadenylation specificity factor 5	AT4G29820
VIT_11s0016g01770	MKK2	AT4G29810
VIT_11s0016g01780	HAB1 (homology toABI1)	AT1G72770
VIT_11s0016g01790	Unknown protein	AT4G29790
VIT_11s0016g01800	Protein kinase MK6	AT4G33080
VIT_11s0016g01810	Unknown protein	AT5G12010
VIT_11s0016g01820	Lactoylglutathione lyase	AT5G57040
VIT_11s0016g01830	Protein kinase	AT2G19410
VIT_11s0016g01840	No hit	-
VIT_11s0016g01850	Anthocyanidin-3-glucoside rhamnosyltransferase	AT5G49690
VIT_11s0016g01860	RPS2 (resistant to p. syringae 2)	AT4G26090
VIT_11s0016g01870	Dihydrolipoamide S-acetyltransferase	AT1G54220
VIT_11s0016g01890	Telomere repeat binding factor 1	AT1G72740
VIT_11s0016g01900	N-MYRISTOYLtransferase	AT5G57020
VIT_11s0016g01910	THO complex subunit 6	AT2G19430
VIT_11s0016g01920	EIF-4A3	AT1G54270
VIT_11s0016g01930	Diacylglycerol acyltransferase	AT2G19450
VIT_11s0016g01940	Unknown protein	AT2G19460
VIT_11s0016g01950	Casein kinase I delta	AT1G72710
VIT_11s0016g02380	1-aminocyclopropane-1-carboxylate oxidase 2 (ACO1)	AT2G19590
VIT_11s0016g02400	K+ efflux antiporter (KEA4)	AT2G19600
VIT_11s0016g02410	MYB divaricata	AT5G56840
VIT_11s0016g02420	UDP-N-acetylglucosamine O-acyltransferase protein	AT4G29540
VIT_11s0016g02430	Dual-specific kinase DSK1	AT3G13690
VIT_11s0016g03130	Ceramide glucosyltransferase	AT2G19880

VIT_11s0016g03140	ERD7 (EARLY-responsive TO dehydration 7)	AT3G21600
VIT_11s0016g03150	TRNA a64-2'-o-ribosylphosphate transferase	AT2G40570
VIT_11s0016g03160	ABC transporter B member 11	AT3G28345
VIT_11s0016g03170	Arabidopsis histidine phosphotransfer AHP4	AT3G16360
VIT_11s0016g03180	ABI1 (ABA insensitive 1)	AT4G26080
VIT_11s0037g01210	Eceriferum 1 (CER1 protein) Sterol desaturase	AT5G57800
VIT_11s0052g00160	ATP binding, related	AT4G29920
VIT_11s0052g00170	Armadillo-like helical domain-containing	AT3G28430
VIT_12s0055g01150	Brassinosteroid insensitive 1-associated receptor kinase 1	AT4G33430
VIT_12s0055g01160	Brassinosteroid insensitive 1-associated receptor kinase 1	AT4G33430
VIT_12s0057g00620	Receptor Like Protein 6	AT1G47890
VIT_12s0057g00630	LHCB2.1 (Photosystem II light harvesting complex gene 2.1)	AT2G05100
VIT_12s0057g00640	Pentatricopeptide (PPR) repeat-containing	AT5G48910
VIT_12s0057g00650	fertility restorer homologue	AT5G65560
VIT_12s0057g00670	Heat shock protein 90C	AT3G07770
VIT_12s0057g00680	Constans interacting protein 6	AT5G48160
VIT_12s0057g00690	Histidine kinase (AHK2)	AT5G35750
VIT_12s0057g00700	Glucan endo-1,3-beta-glucosidase 3 precursor	AT5G35740
VIT_12s0057g00710	DnaJ homolog, subfamily B, member 12	AT2G05230
VIT_12s0057g00720	F-box protein GID2	AT5G48170
VIT_12s0057g00730	No hit	-
VIT_12s0057g00740	Pentatricopeptide (PPR) repeat-containing protein	AT4G26680
VIT_12s0057g00750	CF9	AT1G45616
VIT_12s0057g00760	CF9	AT1G45616
VIT_12s0057g00780	Disease resistance protein	AT3G28890
VIT_12s0057g00800	Receptor Like Protein 27	AT1G47890
VIT_12s0057g00810	Serine-threonine protein kinase	-
VIT_12s0057g00820	Leucine-rich repeat	AT1G45616
VIT_12s0057g00860	CF9	AT3G11010
VIT_12s0057g00870	CF9	AT3G11010
VIT_12s0057g00880	TAF15b (TBP-associated factor 15b) zf-ranBP	AT5G58470
VIT_12s0057g00890	Glycosyl hydrolase family 17 protein	AT5G58480
VIT_12s0057g00900	Import inner membrane translocase subunit TIM50	AT1G55900
VIT_12s0057g00910	Sterile apetala	AT5G35770
VIT_12s0057g00920	Transcriptional adapter ADA2a	AT3G07740
VIT_12s0057g00930	Hydroxycinnamoyl-CoA:shikimate hydroxycinnamoyltransferase	AT5G41040
VIT_12s0057g00940	Glucose-6-phosphate 1-dehydrogenase 2, chloroplast precursor	AT5G35790
VIT_12s0057g00950	No hit	-
VIT_12s0057g00960	FAR1-related sequence 10	AT5G28530
VIT_12s0057g00970	Pentatricopeptide (PPR) repeat-containing	AT5G09950

VIT_12s0057g00980	Phytochrome defective C (PHYC)	AT5G35840
VIT_12s0057g00990	Beta 1,2 N-acetylglucosaminyltransferase	AT2G05320
VIT_12s0057g01000	Unknown protein	AT4G13500
VIT_12s0057g01010	Nuclear transcription factor Ysubunit B-3	AT4G14540
VIT_12s0057g01020	fasciclin-like arabinogalactan protein FLA2	AT4G12730
VIT_12s0057g01030	Glucose-6-phosphate 1-dehydrogenase 2, chloroplast precursor	AT5G35790
VIT_12s0057g01040	No hit	-
VIT_12s0057g01050	Unknown	-
VIT_12s0057g01060	Jasmonate O-methyltransferase	AT3G11480
VIT_12s0057g01070	S-adenosyl-L-methionine: salicylic acid carboxyl methyltransferase	AT3G11480
VIT_12s0057g01080	Kelch repeat-containing protein	AT3G07720
VIT_12s0057g01090	Nudix hydrolase 2	AT5G47650
VIT_12s0057g01100	Nudix hydrolase 2	AT5G47650
VIT_12s0057g01110	Nudix hydrolase 2	AT5G47650
VIT_12s0057g01120	No hit	-
VIT_12s0057g01130	R protein disease resistance protein	AT3G07040
VIT_12s0057g01140	AarF domain containing kinase	AT3G07700
VIT_12s0057g01150	AarF domain containing kinase	AT3G07700
VIT_12s0057g01160	AarF domain containing kinase	AT3G07700
VIT_12s0057g01170	Pentatricopeptide (PPR) repeat-containing protein	AT5G61990
VIT_12s0057g01180	Lipase class 3	AT5G50890
VIT_12s0057g01190	No hit	-
VIT_14s0006g01150	ATP-binding cassette, sub-family F, member 1	-
VIT_14s0006g01170	ATP-dependent RNA helicase A	AT2G35920
VIT_14s0006g01180	ATP-dependent RNA helicase A	AT2G35920
VIT_14s0006g01190	No hit	-
VIT_14s0006g01200	Adenine phosphoribosyltransferase	-
VIT_14s0030g00030	Glutathione synthetase, chloroplast precursor	AT5G27380
VIT_14s0030g00040	Disease resistance protein (CC-NBS-LRR class)	-
VIT_14s0030g00080	No hit	-
VIT_14s0030g00850	No hit	-
VIT_14s0030g00860	No hit	-
VIT_14s0030g00870	CC-NBS-LRR class	-
VIT_14s0030g00880	No hit	-
VIT_14s0030g00890	No hit	-
VIT_14s0030g00900	MRP-like ABC transporter MRP6	-
VIT_14s0030g00910	SOD Cu/Zn superoxide dismutase	-
VIT_14s0030g00920	Alcohol dehydrogenase	-
VIT_14s0030g00930	Laccase	-
VIT_14s0030g00950	SOD Cu/Zn superoxide dismutase	-

VIT_14s0030g00960	R protein MLA10	AT4G27190
VIT_14s0030g00970	Oxidoreductase, zinc-binding dehydrogenase family	-
VIT_14s0030g00980	DNA-directed RNA polymerase III subunit C25	AT1G06790
VIT_14s0030g00990	R protein disease resistance protein	AT4G27190
VIT_14s0030g01000	No hit	-
VIT_14s0030g01020	No hit	-
VIT_14s0030g01030	Alcohol dehydrogenase	-
VIT_14s0030g01040	No hit	-
VIT_14s0030g01050	R protein disease resistance protein	AT4G27190
VIT_14s0030g01060	No hit	-
VIT_14s0030g01070	No hit	-
VIT_14s0081g00150	Ankyrin	AT3G04710
VIT_14s0083g00930	BIM2 (BES1-interacting Myc-like protein 2)	AT1G69010
VIT_14s0083g00940	Auxin-independent growth promoter	AT5G15740
VIT_14s0083g00950	U3 small nucleolar RNA-associated protein IMP3	AT5G15750
VIT_14s0083g00960	Auxin transport protein (BIG)	AT3G02260
VIT_14s0083g00970	Ribosomal protein L7A (RPL7aB) 60S	AT3G62870
VIT_14s0083g00980	Pollen Ole e 1 allergen and extensin	AT5G15780
VIT_14s0083g00990	IMP dehydrogenase	AT5G38880
VIT_14s0083g01000	Zinc finger (C3HC4-type ring finger)	AT3G02290
VIT_14s0083g01010	Protein disulfide oxidoreductase DSBA oxidoreductase	AT5G38900
VIT_14s0083g01020	Regulator of chromosome condensation (RCC1)	AT3G02300
VIT_14s0128g00380	Yip1 domain, member 1	AT5G27490
VIT_14s0128g00390	Mitochondrial FAD carrier	AT3G05290
VIT_14s0128g00400	Ras homolog gene family, member T1	AT5G27540
VIT_15s0021g00880	ferredoxin-related	AT1G02180
VIT_15s0021g00890	Ring-H2 zinc finger protein ATL4	AT3G60220
VIT_15s0021g00900	No hit	-
VIT_15s0021g00910	Dolichyl pyrophosphate Glc1Man9GlcNAc2 alpha-1,3-glucosyltransferase	AT2G44660
VIT_15s0021g00920	ATP synthase delta' chain, mitochondrial	AT5G47030
VIT_15s0021g00930	EMB2745 (embryo defective 2745)	AT5G39710
VIT_15s0021g00990	LOL3 (LSD ONE like 3)	AT1G02170
VIT_15s0021g01000	Ribosomal protein L37a (RPL37aB) 60S	AT3G10950
VIT_15s0021g01010	Phosphatidylinositol-4-phosphate 5-kinase	AT2G35170
VIT_15s0021g01020	Casein kinase II subunit beta-2	AT2G44680
VIT_15s0021g01040	CYP72A1	AT5G24910
VIT_15s0021g01050	No hit	-
VIT_15s0021g01060	CYP72A1	AT5G24910
VIT_15s0045g00930	Unknown	-
VIT_15s0045g00940	No hit	-

VIT_15s0045g00950	No hit	-
VIT_15s0045g00980	R protein PRF disease resistance protein	AT1G50180
VIT_15s0045g01010	R protein PRF disease resistance protein	AT1G50180
VIT_15s0045g01020	R protein PRF disease resistance protein	AT5G43470
VIT_15s0045g01030	MRP-like ABC transporter MRP6	-
VIT_15s0045g01040	KH domain-containing protein	AT2G38610
VIT_18s0001g14690	Protein kinase	AT1G77280
VIT_18s0001g14700	Unknown	-
VIT_18s0001g14710	Ketol-acid reductoisomerase precursor	AT3G58610
VIT_18s0001g14720	Ankyrin repeat family protein	-
VIT_18s0001g14730	Glutaredoxin	AT5G42150
VIT_18s0001g14740	Protein binding	-
VIT_18s0001g14750	Zinc finger (FYVE type) VPS19	AT1G20110
VIT_18s0001g14760	Lipase 3 (EXL3) family II extracellular	AT1G75900
VIT_18s0001g14770	Lipase 3 (EXL3) family II extracellular	AT1G75900
VIT_18s0001g15230	Unknown	-
VIT_18s0001g15240	Blue (type 1) copper domain	AT2G02850
VIT_18s0001g15250	Unknown	-
VIT_18s0001g15260	Myb domain protein 52	AT1G17950
VIT_18s0001g15270	SCL1 (scarecrow-like 1)	AT1G21450
VIT_18s0001g15280	RNA exonuclease 1	AT5G25800
VIT_18s0001g15290	Ribosome maturation protein SDO1	AT1G43860
VIT_18s0001g15300	No hit	-
VIT_18s0001g15310	Thioredoxin M-type	AT3G15360
VIT_18s0001g15320	SEU3B protein	AT1G43850
VIT_18s0001g15330	SWEET1	AT1G21460
VIT_18s0001g15340	Pentatricopeptide (PPR) repeat-containing protein	-
VIT_18s0001g15350	Pentatricopeptide (PPR) repeat-containing protein	AT3G21470
VIT_18s0001g15360	Thylakoid lumenal 29.8 kDa protein	AT1G77090
VIT_18s0001g15370	Exostosin family protein	AT1G21480
VIT_18s0001g15380	No hit	-
VIT_18s0001g15390	Gaiacol peroxidase	AT4G25980
VIT_18s0001g15400	KOW domain-containing transcription factor family protein	AT4G08350
VIT_18s0001g15410	Alcohol dehydrogenase 1	AT1G77120
VIT_18s0001g15420	Auxin efflux carrier protein 6	AT1G77110

CLR_ *sylvestris*		
Gene stable ID	**Functional_annotation**	**Arabidopsis homolog**
VIT_02s0012g02570	Guanine nucleotide-binding protein alpha-1 subunit	AT1G31930
VIT_02s0012g02580	No hit	-
VIT_02s0012g02590	Galacturonosyltransferase 1	-
VIT_02s0012g02600	Octicosapeptide/Phox/Bem1p (PB1) domain-containing protein	-
VIT_02s0012g02610	SAR1 (suppressor of auxin resistance1) (Nup160)	-
VIT_02s0012g02620	PFT1 (phytochrome and flowering time 1) MED25	-
VIT_02s0012g02640	Aspartic-type endopeptidase	-
VIT_02s0012g02650	Purple acid phosphatase 2 PAP2	-
VIT_02s0012g02660	Proteasome 26S regulatory subunit (RPN9)	AT5G45620
VIT_02s0012g02670	Unknown protein	AT1G31940
VIT_02s0012g02680	No hit	-
VIT_02s0012g02690	No hit	-
VIT_02s0025g02890	Ribosomal protein L11	AT1G32990
VIT_02s0025g02900	Zinc transporter MTPA2	AT3G58810
VIT_02s0025g02920	Quercetin 3-O-methyltransferase 1	AT5G54160
VIT_02s0025g02930	Caffeic acid O-3-methyltransferase	AT5G54160
VIT_02s0025g02940	Caffeic acid O-3-methyltransferase	AT5G54160
VIT_02s0025g02960	Naringenin,2-oxoglutarate 3-dioxygenase	AT4G10490
VIT_02s0033g00230	Unknown protein	AT5G48790
VIT_02s0033g00240	Glucosyltransferase twi1	AT2G36780
VIT_13s0073g00120	Ribosomal protein S17 (RPS17A) 40S	AT5G04800
VIT_13s0073g00130	Pentatricopeptide (PPR) repeat membrane-associated salt-inducible protein	AT5G04810
VIT_13s0073g00140	Ovate family protein 13 OFP13	AT5G04820
VIT_13s0073g00150	Heat shock protein-related	AT3G52490
VIT_13s0073g00160	Unknown protein	AT5G04830
VIT_13s0073g00170	Exocyst subunit EXO70 A1	AT5G03540
VIT_13s0073g00320	Poly(A) polymerase	AT4G32850
VIT_13s0073g00380	BHLH038/ORG2 (OBP3-responsive gene 2)	AT3G56970
VIT_13s0073g00390	No hit	-
VIT_13s0073g00400	BHLH038/ORG2 (OBP3-responsive gene 2)	AT3G56970
VIT_13s0073g00410	Nucleolar essential protein	-
VIT_13s0073g00430	BZIP transcription factor	AT5G04840
VIT_13s0073g00440	BSU1-like protein 3 BSL3	AT2G27210
VIT_13s0106g00360	Non-symbiotic hemoglobin class 1	AT2G16060
VIT_13s0106g00370	Myb family	-
VIT_13s0106g00380	Phosphoacetylglucosamine mutase	AT5G18070

VIT_13s0106g00390	VAP27-1 (VAMP/synaptobrevin-associated protein 27-1)	-
VIT_13s0106g00400	Vesicle associated protein VAP	-
VIT_13s0106g00410	Heat shock protein 81-4 (HSP81-4)	-
VIT_13s0106g00420	Metalloendopeptidase	-
VIT_13s0106g00430	Auxin response factor ARF6	AT1G30330
VIT_16s0013g01030	Ethylene-responsive transcription factor ERF105	AT5G51190
VIT_16s0013g01040	No hit	-
VIT_16s0013g01050	Ethylene-responsive transcription factor ERF105	AT4G17490
VIT_16s0013g01060	Ethylene-responsive transcription factor ERF105	AT4G17490
VIT_16s0013g01070	Ethylene-responsive transcription factor ERF105	AT5G51190
VIT_16s0013g01080	Ethylene-responsive transcription factor ERF105	AT5G51190
VIT_16s0013g01090	Ethylene-responsive transcription factor ERF105	AT5G61600
VIT_16s0013g01110	Ethylene-responsive transcription factor 5	AT5G47230
VIT_16s0100g00760	Stilbene synthase 2 [Vitis sp. cv. 'Norton']	AT5G13930
VIT_16s0100g00770	Stilbene synthase	AT5G13930
VIT_16s0100g00780	Stilbene synthase	AT5G13930
VIT_16s0100g00800	Stilbene synthase 4	AT5G13930
VIT_16s0100g00810	Stilbene synthase [Vitis vinifera]	AT5G13930
VIT_16s0100g00830	Stilbene synthase	AT5G13930
VIT_16s0100g00840	Stilbene synthase 4	AT5G13930
VIT_16s0100g00850	Stilbene synthase	AT5G13930
VIT_16s0100g00860	Chalcone synthase	-
VIT_16s0100g00870	No hit	-
VIT_16s0100g00880	Stilbene synthase [Vitis pseudoreticulata]	AT5G13930
VIT_16s0100g00900	Stilbene synthase [Vitis pseudoreticulata]	AT5G13930
VIT_16s0100g00910	Stilbene synthase - grape	AT5G13930
VIT_16s0100g00920	Stilbene synthase - grape	AT5G13930
VIT_16s0100g00930	Stilbene synthase 2	-
VIT_16s0100g00940	Stilbene synthase 3 [Vitis sp. cv. 'Norton']	AT5G13930
VIT_16s0100g00950	Stilbene synthase 3	AT5G13930
VIT_16s0100g00960	Stilbene synthase [Vitis pseudoreticulata]	AT5G13930
VIT_16s0100g00970	No hit	-
VIT_16s0100g00990	Stilbene synthase 2	-
VIT_16s0100g01000	Stilbene synthase 4	-
VIT_16s0100g01010	Stilbene synthase	AT5G13930
VIT_16s0100g01020	Stilbene synthase [Vitis pseudoreticulata]	AT5G13930
VIT_16s0100g01030	Stilbene synthase [Vitis quinquangularis]	AT5G13930
VIT_16s0100g01040	Stilbene synthase - grape	AT5G13930
VIT_16s0100g01060	Stilbene synthase	AT5G13930
VIT_16s0100g01070	Resveratrol synthase [Vitis vinifera]	AT5G13930

VIT_16s0100g01080	No hit	-
VIT_17s0000g10050	Phosphopantothenoylcysteine decarboxylase	AT3G18030
VIT_17s0000g10200	Steroid sulfotransferase	AT2G03760
VIT_17s0000g10210	Unknown protein	AT3G48470
VIT_17s0000g10240	Isocitrate dehydrogenase [NADP]	AT3G48480
VIT_17s0000g10250	Proteasome 26S regulatory subunit (RPN7)	AT4G24820
VIT_17s0000g10260	AarF domain containing kinase	AT4G24810
VIT_17s0000g10420	DNA-binding protein GT-1-related	AT1G13450
VIT_17s0000g10430	Glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3	AT1G13440
VIT_17s0119g00070	Unknown protein	AT3G17800
VIT_17s0119g00080	Organic cation transport protein OCT1	AT1G73220
VIT_17s0119g00090	Unknown protein	AT1G73240

F_{ST} wild &Cultivated		
Gene stable ID	**Functional annotation**	**Arabidopsis homolog**
VIT_02s0012g00010	No hit	-
VIT_02s0012g00020	Glycine-rich protein	AT4G17620
VIT_02s0012g00030	Unknown	-
VIT_02s0012g00040	No hit	-
VIT_02s0012g00050	Glycine-rich protein	AT4G17620
VIT_02s0012g00060	Unknown	-
VIT_02s0012g00070	Unknown protein	AT5G47090
VIT_02s0012g00080	Casein kinase II subunit beta-4	AT4G17640
VIT_02s0012g00090	Phosphatidylinositol-4-phosphate 5-kinase	AT2G35170
VIT_02s0012g00100	Ribosomal protein L37a (RPL37aB) 60S	AT3G10950
VIT_02s0012g00110	Chromatin remodeling 31	AT1G05490
VIT_02s0012g00140	Novel plant snare 11	AT2G35190
VIT_02s0012g02570	Guanine nucleotide-binding protein alpha-1 subunit	AT1G31930
VIT_02s0012g02580	No hit	-
VIT_02s0012g02590	Galacturonosyltransferase 1	-
VIT_02s0012g02600	Octicosapeptide/Phox/Bem1p (PB1) domain-containing protein	-
VIT_02s0012g02610	SAR1 (suppressor of auxin resistance1) (Nup160)	-
VIT_02s0012g02620	PFT1 (phytochrome and flowering time 1) MED25	-
VIT_02s0012g02640	Aspartic-type endopeptidase	-
VIT_02s0012g02650	Purple acid phosphatase 2 PAP2	-
VIT_02s0012g02660	Proteasome 26S regulatory subunit (RPN9)	AT5G45620
VIT_02s0012g02670	Unknown protein	AT1G31940
VIT_02s0012g02680	No hit	-
VIT_02s0012g02690	No hit	-
VIT_02s0012g02700	Unknown	-
VIT_02s0012g02710	Unknown	-
VIT_02s0012g02720	RPM1 (resistance to p. syringae pv maculicola 1)	AT3G07040
VIT_02s0012g02760	Methionyl-tRNA synthetase	AT4G13780
VIT_02s0012g02770	ABC transporter g family pleiotropic drug resistance 12 PDR12	AT1G15520
VIT_02s0012g02780	Cytochrome b5 domain-containing protein	AT4G14965
VIT_02s0012g02790	Secretory carrier membrane protein (SCAMP4)	AT1G32050
VIT_02s0012g02800	No hit	-
VIT_02s0012g02810	CYP76C4	AT2G45550
VIT_02s0012g02820	Geraniol 10-hydroxylase	AT2G45550
VIT_02s0012g02830	UDP-glucosyl transferase	AT3G02100
VIT_02s0012g02840	No hit	-
VIT_02s0154g00010	Auxin-responsive SAUR11	AT3G60690

VIT_02s0154g00020	Vascular related NAC-domain protein 4	AT1G12260
VIT_02s0154g00030	No hit	-
VIT_02s0154g00040	Thylakoid lumenal protein	AT1G12250
VIT_02s0154g00050	Glycosyl hydrolase family 5	AT1G13130
VIT_02s0154g00060	Thylakoid lumenal protein	-
VIT_02s0154g00070	Abnormal floral organs	AT2G45190
VIT_02s0154g00080	Multi-copper oxidase (SKU5)	AT4G12420
VIT_02s0154g00090	Vacuolar invertase 2, GIN2	AT1G12240
VIT_02s0154g00100	Transaldolase totaL2	AT1G12230
VIT_02s0154g00110	Trehalose-6-phosphate phosphatase (AtTPPA)	AT4G12430
VIT_02s0154g00120	Unknown	AT4G22600
VIT_02s0154g00130	Exostosin (Xyloglucan galactosyltransferase KATAMARI 1)	AT4G22580
VIT_02s0154g00140	3-oxoacyl-[acyl-carrier-protein] synthase 3 A, chloroplast precursor	AT1G62640
VIT_02s0154g00150	PLATZ transcription factor	AT3G60670
VIT_02s0154g00160	flavin-containing monooxygenase family protein / FMO family protein	AT1G62600
VIT_02s0154g00170	flavin-containing monooxygenase 3	-
VIT_02s0154g00180	flavin-containing monooxygenase 3	AT1G62600
VIT_02s0154g00190	flavin-containing monooxygenase 3	AT1G62620
VIT_02s0154g00200	Unknown protein	AT1G12120
VIT_02s0154g00210	WRKY DNA-binding protein 21	AT2G30590
VIT_02s0154g00220	Zinc finger (C2H2 type) family	AT1G62520
VIT_02s0154g00230	Phosphatidic acid phosphatase / PAP2	AT4G22550
VIT_02s0154g00240	Oxysterol binding protein	AT4G22540
VIT_02s0154g00250	Oxysterol binding protein	AT4G22540
VIT_02s0154g00260	Nitrate transporter	AT1G12110
VIT_02s0154g00270	No hit	-
VIT_02s0154g00280	Arachidonic acid-induced DEA1	AT1G12090
VIT_02s0154g00290	Extensin	AT4G12510
VIT_02s0154g00300	Small nuclear ribonucleoprotein Sm D3	AT1G12090
VIT_02s0154g00310	Protease inhibitor/seed storage/lipid transfer protein (LTP)	AT1G62500
VIT_02s0154g00320	Protease inhibitor/seed storage/lipid transfer protein (LTP)	AT2G45180
VIT_02s0154g00330	Unknown protein	AT5G47570
VIT_02s0154g00340	No hit	-
VIT_02s0154g00350	L-lactate dehydrogenase A	AT4G17260
VIT_02s0154g00360	No hit	-
VIT_02s0154g00370	YbaK/prolyl-tRNA synthetase associated region	AT4G16510
VIT_02s0154g00380	Unknown	-
VIT_02s0154g00390	Autophagy 8f (APG8f)	AT4G16520
VIT_02s0154g00400	Scarecrow transcription factor 6 (SCL6)	AT4G00150

VIT_02s0154g00410	Unknown protein	AT5G47580
VIT_02s0154g00420	No hit	-
VIT_02s0154g00430	Unknown	-
VIT_02s0154g00440	Unknown protein	AT5G47580
VIT_02s0154g00450	Zinc knuckle	-
VIT_02s0154g00460	Unknown protein	AT4G16530
VIT_02s0154g00470	No hit	-
VIT_02s0154g00480	Heat shock protein MTSHP	AT4G25200
VIT_02s0154g00490	Heat shock 22 kDa protein mitochondrial	AT4G25200
VIT_02s0154g00500	VAP27-1 (VAMP/synaptobrevin-associated protein 27-1)	AT3G60600
VIT_02s0154g00510	SEC14 cytosolic factor	AT5G47510
VIT_02s0154g00520	Aspartyl protease	AT4G16563
VIT_02s0154g00530	Histidine triad nucleotide binding protein 3	AT4G16566
VIT_02s0154g00540	Protein arginine N-methyltransferase	AT4G16570
VIT_02s0154g00550	DnaJ homolog, subfamily C, member 11	AT2G35720
VIT_02s0154g00560	No hit	-
VIT_02s0154g00580	Unknown	-
VIT_02s0154g00590	Unknown	-
VIT_02s0154g00600	Pectinesterase family	AT5G47500
VIT_02s0154g00610	Pex19 protein	AT5G17550
VIT_02s0154g00620	Unknown	-
VIT_02s0236g00010	Unknown	-
VIT_02s0236g00020	Unknown	-
VIT_02s0236g00030	Unknown	-
VIT_02s0236g00040	Peptidyl-prolyl cis-trans isomerase, cyclophilin type	AT4G17070
VIT_02s0236g00050	Unknown	-
VIT_02s0236g00060	Unknown	-
VIT_02s0236g00070	Unknown	-
VIT_02s0236g00080	Ribosomal protein P0 acidic	-
VIT_02s0236g00090	Unknown	-
VIT_02s0236g00100	Unknown	-
VIT_02s0236g00110	No hit	-
VIT_02s0236g00120	Unknown	-
VIT_02s0236g00130	SNF1-related protein kinase SRK2F	AT4G33950
VIT_02s0236g00140	Calcineurin B 1	-
VIT_02s0236g00150	Calcineurin B 1	AT4G17615
VIT_02s0236g00160	Serine/threonine Phosphatase 7	-
VIT_02s0236g00170	No hit	-
VIT_02s0241g00070	Zinc finger (DHHC type)	AT3G60800
VIT_02s0241g00080	Glycine-rich protein-like	AT4G22740

VIT_02s0241g00090	Translation release factor	AT1G62850
VIT_02s0241g00100	Unknown protein	AT2G45360
VIT_02s0241g00110	Aminomethyltransferase	AT4G12130
VIT_02s0241g00120	Receptor protein kinase	AT4G22730
VIT_02s0241g00130	No hit	-
VIT_02s0241g00140	Calmodulin (A)	AT1G12310
VIT_02s0241g00150	No hit	-
VIT_02s0241g00160	Esterase/lipase/thioesterase family	AT4G12230
VIT_02s0241g00170	Zinc finger (C2H2 type) family	AT4G12240
VIT_02s0241g00180	UDP-D- glcucuronate 4-epimerase 5 GAE5	AT4G12250
VIT_02s0241g00190	No hit	-
VIT_02s0488g00010	H (+)-ATPase 4 AHA4	AT5G62670
VIT_02s0488g00020	Palmitoyl-protein thioesterase 1 precursor	AT3G60340
VIT_02s0488g00030	No hit	-
VIT_02s0488g00040	Pentatricopeptide repeat-containing protein	-
VIT_02s0488g00050	Dual specificity phosphatase	-
VIT_04s0008g00030	Unknown	-
VIT_04s0008g00050	Ribosomal protein L5-1 60S	-
VIT_04s0008g00060	Proteasome 26S regulatory subunit S5A (RPN10)	-
VIT_04s0008g00080	No hit	-
VIT_04s0008g00130	Avr9/Cf-9 rapidly elicited protein 146	AT1G52140
VIT_04s0008g00160	Casein kinase	AT2G25760
VIT_04s0008g00170	Retrotransposon protein, Unclassified	AT1G15215
VIT_04s0008g00180	NADP-dependent malic enzyme	AT1G79750
VIT_04s0008g00190	ATP-dependent protease La (LON) domain-containing	AT2G25740
VIT_04s0008g00200	Tryptophan-tRNA ligase	AT2G25840
VIT_04s0008g00210	Histidine-containing phosphotransferase	AT3G16360
VIT_04s0008g00220	IAA6	AT3G16500
VIT_04s0008g00230	Amino acid permease 8	AT1G10010
VIT_04s0008g00240	Amino acid permease 6	AT5G49630
VIT_04s0008g00250	Amino acid permease 6	AT5G49630
VIT_04s0008g00260	Amino acid permease 6	AT5G49630
VIT_04s0008g00270	Elongation factor 1-alpha (EF-1-alpha)	AT5G60390
VIT_04s0008g00280	Amino acid permease 1	AT1G58360
VIT_04s0008g00290	Clavata1 receptor kinase (CLV1)	AT5G25930
VIT_04s0008g00300	Clavata1 receptor kinase (CLV1)	AT5G25930
VIT_04s0008g00310	Clavata1 receptor kinase (CLV1)	AT5G25930
VIT_04s0008g00320	Leucine-rich repeat family protein	-
VIT_04s0008g00330	Clavata1 receptor kinase (CLV1)	AT5G25930
VIT_04s0008g00340	Clavata1 receptor kinase (CLV1)	AT5G25930

VIT_04s0008g00350	Clavata1 receptor kinase (CLV1)	AT5G25930
VIT_04s0008g00370	Clavata1 receptor kinase (CLV1)	AT5G25930
VIT_04s0008g00380	No hit	-
VIT_04s0008g00390	Clavata1 receptor kinase (CLV1)	AT5G25930
VIT_04s0008g00400	Clavata1 receptor kinase (CLV1)	AT5G25930
VIT_04s0008g00410	Clavata1 receptor kinase (CLV1)	AT5G25930
VIT_04s0008g00420	Clavata1 receptor kinase (CLV1)	AT5G25930
VIT_04s0008g00430	Clavata1 receptor kinase (CLV1)	AT5G25930
VIT_04s0008g00440	Clavata1 receptor kinase (CLV1)	AT5G25930
VIT_04s0008g00450	Haloacid dehalogenase hydrolase	AT2G25870
VIT_04s0008g00460	Unknown protein	AT5G56550
VIT_04s0008g00470	Early nodulin Enod93 protein	-
VIT_04s0008g00480	Pentatricopeptide (PPR) repeat-containing	AT5G48910
VIT_04s0008g00490	Profilin 5 (PRO5) (PRF3)	AT5G56600
VIT_04s0008g00510	Derlin-1	AT4G29330
VIT_04s0008g00520	6-phosphofructokinase	AT4G26270
VIT_04s0008g00530	Serine/threonine-protein kinase Aurora-1	AT4G32830
VIT_04s0008g00540	Oleosin OLE-3	AT2G25890
VIT_04s0008g00550	Unknown protein	AT1G20890
VIT_04s0008g00560	Tetratricopeptide repeat (TPR)-containing	AT4G32820
VIT_04s0008g00570	Glu-tRNA(Gln) amidotransferase subunit C	AT4G32915
VIT_04s0008g00600	RNA polymerase sigma factor SIGC	AT3G53920
VIT_04s0008g00610	Zinc finger (CCCH-type) family protein	AT2G19810
VIT_04s0008g00620	Myb domain protein 68	AT5G65790
VIT_04s0008g00630	SNF7.2	-
VIT_04s0008g00640	Epsin N-terminal homology (ENTH) domain-containing	AT5G11710
VIT_04s0008g00650	3'-5' exonuclease domain-containing protein	AT2G25910
VIT_04s0008g00660	Early flowering 3	AT2G25930
VIT_04s0008g00670	DD1A protein	AT5G25950
VIT_04s0008g00680	Unknown protein	AT4G32930
VIT_04s0008g00690	Unknown protein	AT5G11730
VIT_04s0008g00700	No hit	-
VIT_04s0008g00710	Unknown	-
VIT_04s0008g00720	Vacuolar processing enzyme gamma	AT4G32940
VIT_04s0008g00730	Unknown protein	AT3G20430
VIT_04s0008g00740	Protein phosphatase 2C	AT5G26010
VIT_04s0008g00750	Unknown protein	AT4G32960
VIT_04s0008g00760	Thioredoxin Trp26	AT2G25950
VIT_04s0008g00770	Glycine hydroxymethyltransferase	AT4G32520
VIT_04s0008g00780	Unknown	-

VIT_04s0008g00790	Ribosomal protein L28 (RPL28C) 60S	AT2G19730
VIT_04s0008g00800	Ferrochelatase-2	AT5G26030
VIT_04s0008g00810	ATP synthase g subunit mitochondrial	AT4G29480
VIT_04s0008g00820	KH domain-containing protein	AT2G25970
VIT_04s0008g00830	NADH dehydrogenase (ubiquinone) Fe-S protein 7	AT5G11770
VIT_04s0008g00840	Ser/Thr specific protein phosphatase 2A B regulatory subunit beta isoform	AT1G17720
VIT_04s0008g00850	Unknown	-
VIT_04s0008g00860	Ndr family protein	AT5G11790
VIT_04s0008g00870	Phosphoethanolamine/phosphocholine phosphatase	AT1G17710
VIT_04s0008g00880	Homeobox gene 1	AT4G32980
VIT_04s0008g00890	Abscisic acid receptor PYL2 RCAR14	AT2G26040
VIT_04s0008g00900	MYB divaricata	AT5G56840
VIT_04s0008g00910	Histone deacetylase protein (HDA2)	AT5G26040
VIT_04s0008g00920	Clavata1 receptor kinase (CLV1)	AT5G25930
VIT_04s0008g00930	Alpha-expansin 6 precursor	-
VIT_04s0008g00950	Calcineurin B protein 10	AT4G33000
VIT_04s0008g00960	Calcineurin B protein 10	AT4G33000
VIT_04s0008g00970	Translation initiation factor eIF-4A	-
VIT_04s0008g00980	Translation initiation factor eIF-4A	-
VIT_04s0008g00990	Translation initiation factor eIF-4A	AT3G13920
VIT_04s0008g01000	EIF-4A3	AT3G13920
VIT_04s0008g01010	No hit	-
VIT_04s0008g01020	Unknown protein	AT5G11970
VIT_04s0008g01030	Unknown protein	AT5G11960
VIT_04s0008g01040	Lysine decarboxylase	AT5G11950
VIT_04s0008g01050	Unknown	-
VIT_04s0008g01060	Substrate carrier, Mitochondrial	AT1G14560
VIT_04s0008g01070	Calmodulin-binding region IQD6	AT2G26190
VIT_04s0008g01080	Calmodulin-binding region IQD6	AT2G26180
VIT_04s0008g01090	CYP706A12	AT2G26170
VIT_04s0008g01100	CYP706A12	AT2G26170
VIT_04s0008g01110	Heat shock transcription factor A6B	AT2G26150
VIT_04s0008g01120	Glutaredoxin	AT4G33040
VIT_04s0008g01130	Solute carrier family 25	AT5G56450
VIT_04s0008g01140	Beta-fructosidase (BFRUCT1)	AT3G13790
VIT_04s0008g01150	Beta-fructosidase (BFRUCT1)	AT3G13790
VIT_04s0008g01160	Indeterminate(ID)-domain 7	AT3G13810
VIT_04s0008g01170	FtsH protease that is localized to the mitochondrion	AT2G26140
VIT_04s0008g01180	Esterase	AT5G11910
VIT_04s0008g01190	UDP-sulfoquinovose synthase SQD1	AT4G33030

VIT_04s0008g01200	Eukaryotic translation initiation factor SUI1	AT5G11900
VIT_04s0008g01210	Delta-8 sphingolipid desaturase	AT2G46210
VIT_04s0008g01220	RKL1 (Receptor-like kinase 1)	AT1G68400
VIT_04s0008g01230	Harpin-induced protein	AT1G17620
VIT_04s0008g01240	SAG18 (Senescence associated gene 18)	AT5G11870
VIT_04s0008g01250	Unknown	-
VIT_04s0008g01260	Zinc transporter ZIP4	AT1G10970
VIT_04s0008g01270	Beta-1,3-galactosyltransferase 6	AT2G26100
VIT_04s0008g01280	No hit	-
VIT_04s0008g01290	CGA1 (cytokinin-responsive GATA factor 1)	AT4G26150
VIT_04s0008g01300	Glycine dehydrogenase	AT4G33010
VIT_04s0008g01310	MAP3K delta-1 protein kinase	AT5G11850
VIT_04s0008g01320	Unknown protein	AT5G11840
VIT_04s0008g01330	RTE1 (reversion-to-ethylene sensitivity1)	AT2G26070
VIT_04s0008g01340	Unknown protein	AT5G11810
VIT_04s0008g01350	Conserved oligomeric Golgi complex component 8	AT5G11980
VIT_04s0008g01360	Tassel serine threonine kinase 1	AT5G12000
VIT_04s0008g01370	Peptidyl-prolyl cis-trans isomerase SDCCAG10	AT4G33060
VIT_04s0008g01380	Unknown protein	AT5G12010
VIT_04s0008g01390	RNA recognition motif (RRM)-containing protein	AT1G21312
VIT_04s0008g01400	Protein kinase MK6	AT4G33080
VIT_04s0008g01410	Ran-binding protein 1 RanBP1	AT5G58590
VIT_04s0008g01420	HAB2 (Homology to ABI2)	AT1G17550
VIT_04s0008g01430	APM1 (Aminopeptidase M1)	AT4G33090
VIT_04s0008g01440	UPF0203 protein	AT4G33100
VIT_04s0008g01450	Cyclopropane-fatty-acyl-phospholipid synthase	AT4G33110
VIT_04s0008g01460	Unknown protein	AT5G26160
VIT_04s0008g01470	WRKY DNA-binding protein 50	AT5G26170
VIT_04s0008g01480	NOL1/NOP2/sun family protein	AT5G26180
VIT_04s0008g01490	Heat shock protein 17.6 kDa class II	AT5G12020
VIT_04s0008g01500	Heat shock protein 17.6 kDa class II	AT5G12020
VIT_04s0008g01510	Heat shock protein 17.6 kDa class II	AT5G12020
VIT_04s0008g01520	Heat shock protein 17.6 kDa class II	AT5G12020
VIT_04s0008g01530	Small molecular heat shock protein 17.5	AT5G12020
VIT_04s0008g01540	No hit	-
VIT_04s0008g01550	Small molecular heat shock protein 17.5	AT5G12020
VIT_04s0008g01560	Small molecular heat shock protein 17.5	AT5G12020
VIT_04s0008g01570	Heat shock protein 17.6 kDa class II	AT5G12020
VIT_04s0008g01580	Heat shock protein 17.6 kDa class II	AT5G12020
VIT_04s0008g01590	Heat shock protein 17.6 kDa class II	AT5G12020

VIT_04s0008g01610	Heat shock protein 17.6 kDa class II	-
VIT_04s0008g01620	Heat shock protein 17.6 kDa class II	-
VIT_04s0008g01630	No hit	-
VIT_04s0008g01640	Ankyrin repeat	-
VIT_04s0008g01650	Ankyrin repeat	AT5G51160
VIT_04s0008g01660	Carrier protein, Mitochondrial	AT1G72820
VIT_04s0008g01670	PHD finger protein alfin	AT5G26210
VIT_04s0008g01680	EMB2745	AT5G39710
VIT_04s0008g01690	Carbon-nitrogen hydrolase	AT5G12040
VIT_04s0008g01700	Unknown protein	AT1G54200
VIT_04s0008g01710	MAP3K delta-1 protein kinase	AT4G38470
VIT_04s0008g01720	Mechanosensitive ion channel	AT5G12080
VIT_04s0008g01730	PSBX (photosystem II subunit X)	-
VIT_04s0008g01740	Spermine synthase ACAULIS5	AT5G19530
VIT_04s0008g01750	Ribosomal protein S3 (RPS3C) 40S	AT5G35530
VIT_04s0008g01760	PEX10 (peroxin 10)	AT2G26350
VIT_04s0008g01770	Molecular chaperone DnaJ	AT5G21430
VIT_04s0008g01780	Transposon protein, putative, CACTA	-
VIT_04s0008g01790	No hit	-
VIT_04s0008g01800	Myb domain protein 7	AT4G38620
VIT_04s0008g01810	Myb domain protein 4	AT4G38620
VIT_04s0008g01820	TT2 (transparent testa 2)	AT5G35550
VIT_04s0008g01830	Myb domain protein 32	AT4G34990
VIT_04s0008g01840	TT2 (transparent testa 2)	AT5G35550
VIT_04s0008g01850	Trihelix DNA-binding protein (GT2)	AT1G76880
VIT_04s0008g01860	CYP72A58	AT3G14690
VIT_04s0008g01870	ATMYB66/WER/WER1 (WEREWOLF 1)	AT5G14750
VIT_04s0008g01880	Cytokinin dehydrogenase 7	AT5G21482
VIT_04s0008g01890	F-box family protein (FBL15)	AT4G33210
VIT_04s0008g01900	Unknown protein	AT2G26340
VIT_04s0008g01910	ferredoxin-related	AT1G02180
VIT_04s0008g01920	F-box/LRR-repeat protein 20	AT2G06040
VIT_04s0008g01940	Unknown	-
VIT_04s0008g01950	YGGT	AT5G21920
VIT_04s0008g01960	Copper-transporting ATPase PAA2	AT5G21930
VIT_04s0008g01970	ER (ERECTA)	AT2G26330
VIT_04s0008g01980	MADS-box agamous-like 30	-
VIT_04s0008g01990	Myosin-like protein XI-I	AT4G33200
VIT_04s0008g02000	Unknown protein	AT5G21940
VIT_04s0008g02010	Endo-1,4-beta-glucanase	AT3G43860

VIT_04s0008g02020	Cellulase	AT3G43860
VIT_04s0008g02030	Unknown protein	AT2G26310
VIT_04s0008g02040	Heterotrimeric G protein alpha subunit	AT2G26300
VIT_04s0008g02050	Hydrolase, alpha/beta fold	AT4G33180
VIT_04s0008g02070	Avr9/Cf-9 induced kinase 1	AT2G05940
VIT_04s0008g02080	GCR1 (G-protein-coupled receptor 1)	AT1G48270
VIT_04s0008g02090	Copper transporter 5	AT1G72510
VIT_04s0008g02100	CID7 damaged DNA binding	AT2G26280
VIT_04s0008g02110	No hit	-
VIT_04s0008g02120	EMB2758 (embryo defective 2758)	AT4G33170
VIT_04s0008g02140	EMB2261 (embryo defective 2261)	AT4G33170
VIT_04s0008g02150	DCL3 (DICER-like 3)	AT3G43920
VIT_04s0008g02170	DCL3 (DICER-like 3)	AT3G43920
VIT_04s0008g02180	BRCT domain-containing protein	AT3G43930
VIT_04s0008g02190	Glutathione synthase S6 modification	-
VIT_04s0008g02200	3-beta-hydroxy-delta5-steroid dehydrogenase	AT2G26260
VIT_04s0008g02210	RPD1 (root primordium defective 1)	AT5G21970
VIT_04s0008g02220	Sterile alpha motif (SAM) domain-containing protein	AT2G45700
VIT_04s0008g02230	AP2 domain-containing transcription factor ORA47	AT1G19210
VIT_04s0008g02240	Ubiquitin thiolesterase	-
VIT_04s0008g02250	Beta-ketoacyl-CoA synthase	AT2G26250
VIT_04s0008g02260	Dimethylaniline monooxygenase (N-oxide forming) 2	AT1G19250
VIT_04s0008g02270	Hydroxyproline-rich glycoprotein	AT5G21280
VIT_04s0008g02280	Unknown protein	AT3G43540
VIT_04s0008g02290	ABI3-interacting protein 2	AT5G20910
VIT_04s0008g02300	Pyruvate dehydrogenase E1 beta subunit	AT5G50850
VIT_04s0008g02310	ABI3-interacting protein 2, AIP2	AT5G20910
VIT_04s0008g02320	Coatomer subunit beta	AT4G31480
VIT_04s0008g02330	Protein tyrosine phosphatase	AT5G10700
VIT_04s0008g02340	Exocyst subunit EXO70 protein	AT4G31540
VIT_04s0008g02350	No hit	-
VIT_04s0008g02360	No hit	-
VIT_04s0008g02370	Pentatricopeptide (PPR) repeat-containing protein	AT5G10690
VIT_04s0008g02380	Kelch repeat-containing F-box protein	AT2G24540
VIT_04s0008g02390	Zinc finger (C3HC4-type ring finger)	AT5G24870
VIT_04s0008g02400	No hit	-
VIT_04s0008g02410	Unknown protein	AT4G31440
VIT_04s0008g02420	No hit	-
VIT_04s0008g02440	Unknown protein	AT5G10710
VIT_04s0008g02450	Unknown protein	AT5G25500

VIT_04s0008g02460	H+-transporting ATPase, Plasma membrane	AT2G24520
VIT_04s0008g02470	No hit	-
VIT_04s0008g02480	Unknown protein	AT4G31430
VIT_04s0008g02490	Adagio protein 1	AT5G57360
VIT_04s0008g02500	Hydroxyproline-rich glycoprotein LKP2	AT2G18910
VIT_04s0008g02510	Receptor kinase homolog LRK10	AT1G70250
VIT_04s0008g02520	ATP binding protein	AT1G34300
VIT_04s0008g02530	ATP binding protein	AT1G34300
VIT_04s0008g02540	Zinc finger (C2H2 type) family	AT4G31420
VIT_04s0008g02550	4-coumarate-CoA ligase	AT4G31410
VIT_04s0008g02560	AarF domain containing kinase	AT4G31390
VIT_04s0008g02570	Replicon protein A (ATRPA2/ROR1/RPA2)	AT2G24490
VIT_04s0008g02580	V-type H+-transporting ATPase subunit A	AT1G78900
VIT_04s0008g02590	Selenoprotein	AT4G31360
VIT_04s0008g02600	fasciclin arabinogalactan-protein (FLA14)	AT3G12660
VIT_04s0008g02610	FPF1 (flowering promoting factor 1)	AT5G10625
VIT_04s0008g02620	Small nuclear ribonucleoprotein	AT4G18372
VIT_04s0008g02630	Unknown protein	AT2G19160
VIT_04s0008g02640	PAP/fibrillin family	AT5G19940
VIT_04s0008g02650	Unknown protein	AT5G10620
VIT_04s0008g02660	Calmodulin-binding protein	AT2G43040
VIT_04s0008g02670	Cryptochrome DASH	AT5G24850
VIT_04s0008g02680	No hit	-
VIT_04s0008g02690	ELM2 domain-containing protein	AT2G19260
VIT_04s0008g02700	TRNA (guanine-N (1)-)-methyltransferase	AT5G24840
VIT_04s0008g02710	NAC domain containing protein 39	AT2G24430
VIT_04s0008g02720	Myosin heavy chain	AT4G31340
VIT_04s0008g02730	No hit	-
VIT_04s0008g02740	AarF domain containing kinase	AT5G24810
VIT_04s0008g02750	BZIP transcription factor BZO2H2	AT5G24800
VIT_04s0008g02760	Unknown protein	AT4G31330
VIT_04s0008g02770	Syntaxin-related protein KNOLLE	AT1G08560
VIT_04s0008g02780	RBR1 (retinoblastoma-related 1)	AT3G12280
VIT_04s0008g02790	Short-chain dehydrogenase/reductase (SDR)	AT5G15940
VIT_04s0008g02800	SAUR_D	AT2G24400
VIT_04s0008g02810	Chaperone protein dnaJ	AT2G24395
VIT_04s0008g02820	Glycosyltransferase family protein 47	-
VIT_04s0008g02830	Galactokinase like protein	AT4G16130
VIT_04s0008g02840	Avirulence induced gene (AIG)	AT2G24390
VIT_04s0008g02850	Proteasome 20S beta subunit A (PBA1) (PRCD)	AT4G31300

VIT_04s0008g02860	Cation transport protein chaC	AT4G31290
VIT_04s0008g02870	Transcription factor	AT4G31270
VIT_04s0008g02880	Extracellular ligand-gated ion channel	AT2G21080
VIT_04s0008g02890	Receptor kinase	AT4G31250
VIT_04s0008g02900	Protein disulfide isomerase	AT4G31240
VIT_04s0008g02910	Tassel serine threonine kinase 1	AT2G24370
VIT_04s0008g02920	Desiccation protein PCC13-62 precursor	AT1G47980
VIT_04s0008g02930	Oligouridylate binding protein 1B UBP1B	AT1G17370
VIT_04s0008g02950	DNA topoisomerase I	AT4G31210
VIT_04s0008g02960	CYP706A12	AT5G36110
VIT_04s0008g02970	Calmodulin-binding protein	AT2G43040
VIT_04s0008g02980	Lupeol synthase	AT1G78955
VIT_04s0008g02990	Cycloartenol synthase	-
VIT_04s0008g03000	Cycloartenol synthase	AT1G78950
VIT_04s0008g03010	Aspartyl-tRNA synthetase	AT4G31180
VIT_04s0008g03020	Serine/threonine/tyrosine kinase DSK2	AT2G24360
VIT_04s0008g03030	RNA recognition motif (RRM)-containing	AT2G24350
VIT_04s0008g03040	RNA recognition motif (RRM)-containing	AT2G24350
VIT_04s0008g03050	Acetylglutamate kinase	AT3G57560
VIT_04s0008g03060	Transducin protein	AT4G31160
VIT_04s0008g03070	No hit	-
VIT_04s0008g03080	Endonuclease V family protein	AT4G31150
VIT_04s0008g03090	Unknown protein	AT4G31130
VIT_04s0008g03100	Unknown protein	AT4G31130
VIT_04s0008g03110	EMB1611	AT2G34780
VIT_04s0008g03120	Protein arginine N-methyltransferase 5	AT4G31120
VIT_04s0008g03130	Unknown protein	-
VIT_04s0008g03140	Unknown	-
VIT_04s0008g03150	S-adenosyl-L-methionine-dependent methyltransferase mraW	AT5G10910
VIT_04s0008g03160	G protein protein gamma subunit (AGG2)	-
VIT_04s0008g03170	Ubiquitin-specific protease 26 (UBP26)	AT3G49600
VIT_04s0008g03180	Unknown protein	AT4G20325
VIT_04s0008g03190	F-box family protein (FBX13)	AT4G33160
VIT_04s0008g03200	Lachrymatory factor synthase	AT4G32870
VIT_04s0008g03210	Lachrymatory factor synthase	AT4G32870
VIT_04s0008g03220	Lysophospholipase	AT5G11650
VIT_04s0008g03230	Unknown protein	AT5G25840
VIT_04s0008g03240	BAM2 (big apical meristem 2)	AT2G25790
VIT_04s0008g03250	Homeobox gene 8	AT4G32880
VIT_04s0008g03260	Thioredoxin domain containing 14	AT5G11640

VIT_04s0008g03270	GATA transcription factor 11	AT5G25830
VIT_04s0008g03280	No hit	-
VIT_04s0008g03290	Peptidyl-tRNA hydrolase 2	AT4G32900
VIT_04s0008g03300	SWIM zinc finger family (MAPKKK)	AT5G11620
VIT_04s0008g03310	Pentatricopeptide (PPR) repeat	AT1G11290
VIT_04s0008g03320	UVB-resistance protein	AT5G11580
VIT_04s0008g03330	Nucleoporin nup85	AT4G32910
VIT_04s0008g03340	No hit	-
VIT_04s0008g03350	Unknown protein	AT2G25800
VIT_04s0008g03360	F-box and leucine-rich repeat protein 20	-
VIT_04s0008g03370	YebC	AT2G25830
VIT_04s0008g03380	Carotenoid cleavage dioxygenase 8	AT4G32810
VIT_04s0008g03390	No hit	-
VIT_04s0008g03400	DREB sub A-4 of ERF/AP2 transcription factor	AT5G11590
VIT_04s0008g03410	Unknown protein	AT5G11600
VIT_04s0008g03420	Exostosin family protein	AT5G25820
VIT_04s0008g03430	Exostosin family	AT5G25820
VIT_04s0008g03440	Exosome complex exonuclease RRP46	AT3G46210
VIT_04s0008g03450	Lignostilbene-alpha, beta-dioxygenase and related enzymes	AT3G63520
VIT_04s0008g03460	Histidine kinase 1 AHK3	AT1G27320
VIT_04s0008g03470	Myb domain protein 109	-
VIT_04s0008g03480	Beta-carotene 15,15'-monooxygenase	AT3G63520
VIT_04s0008g03490	Ankyrin repeat protein	-
VIT_04s0008g03500	Ankyrin	AT1G10340
VIT_04s0008g03510	Lignostilbene-alpha, beta-dioxygenase and related enzymes	AT3G63520
VIT_04s0008g03520	Ring-H2 finger protein ATL4J	-
VIT_04s0008g03530	Ankyrin repeat	AT1G10340
VIT_04s0043g00680	No hit	-
VIT_04s0043g00690	ARR22 Type A	AT3G04280
VIT_04s0043g00700	PTAC3 (plastid transcriptionally active3)	AT3G04260
VIT_04s0043g00710	Hypoxia up-regulated 1 HSP70	AT4G16660
VIT_04s0043g00720	Transketolase	AT2G34590
VIT_04s0043g00730	formamidopyrimidine-DNA glycosylase 1	AT1G52500
VIT_04s0043g00740	Cytoplasmic FMR1 interacting protein	AT5G18410
VIT_04s0043g00750	No hit	-
VIT_04s0043g00760	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase SEC	AT3G04240
VIT_04s0043g00770	Pentatricopeptide (PPR) repeat-containing protein	AT5G18390
VIT_04s0043g00780	Unknown	-
VIT_04s0043g00790	ribulose-1,5 bisphosphate carboxylase oxygenase large subunit N-methyltransferase	AT1G01920

VIT_04s0043g00800	2OG-Fe(II) oxygenase	AT2G36690
VIT_04s0043g00810	No hit	-
VIT_04s0043g00820	Syntaxin 1B/2/3/4	AT2G18260
VIT_04s0043g00830	Unknown protein	AT3G04160
VIT_04s0043g00840	Armadillo/beta-catenin repeat protein / U-box domain-containing protein	AT3G07360
VIT_04s0043g00850	Unknown protein	AT5G18310
VIT_04s0043g00860	Unknown protein	AT2G38430
VIT_04s0043g00870	Unknown protein	AT1G08530
VIT_04s0043g00880	Tyrosine decarboxylase	-
VIT_13s0019g01410	OBP3 (OBF-binding protein 3)	AT5G02460
VIT_13s0019g01430	Heat shock protein 70	AT5G02500
VIT_13s0019g01440	No hit	-
VIT_13s0019g01450	Unknown protein	AT3G04020
VIT_13s0019g01470	Geranylgeranyltransferase type I beta subunit	AT2G39550
VIT_13s0019g01490	C2 domain-containing protein	AT3G55470
VIT_13s0019g01510	Unknown protein	AT2G39690
VIT_13s0019g01530	Adaptor-related protein complex 3, beta 2 subunit	AT3G55480
VIT_13s0019g01570	Unknown protein	AT5G54440
VIT_13s0019g01590	Pentatricopeptide repeat-containing protein	-
VIT_13s0019g01600	No hit	-
VIT_13s0019g01610	XH/XS domain-containing protein	AT3G48670
VIT_13s0019g01620	No hit	-
VIT_13s0019g01640	Unknown protein	AT1G13790
VIT_13s0019g01650	Alpha-expansin 6 precursor	AT2G39700
VIT_13s0019g01670	Telomeric DNA binding protein 1	AT5G13820
VIT_13s0019g01700	Scarecrow transcription factor 14 (SCL14)	AT1G07530
VIT_13s0019g01710	Scarecrow transcription factor 14 (SCL14)	AT1G07530
VIT_13s0019g01740	Scarecrow transcription factor 14 (SCL14)	AT1G07530
VIT_13s0019g01780	Scarecrow transcription factor 14 (SCL14)	AT1G07530
VIT_13s0019g01790	Scarecrow transcription factor 14 (SCL14)	AT1G07530
VIT_13s0019g01810	Scarecrow transcription factor 14 (SCL14)	AT1G07530
VIT_13s0019g01820	Cell division protein methyltransferase FtsJ	AT5G13830
VIT_13s0019g01840	Cell division cycle 20-like protein 1	AT5G13840
VIT_13s0019g01860	Actin-related protein 5	AT3G12380
VIT_13s0019g01870	No hit	-
VIT_13s0019g01890	DVL11/RTFL8 (ROTUNDIFOLIA like 8)	AT2G39705
VIT_13s0019g01900	FK506-binding protein 4/5	AT3G55520
VIT_13s0019g01920	Laccase	AT5G60020
VIT_13s0019g01930	Laccase	AT5G60020
VIT_13s0019g01940	Laccase	AT5G60020

VIT_13s0019g01960	Zinc finger (C3HC4-type ring finger)	AT3G55530
VIT_13s0019g01970	No hit	-
VIT_13s0019g01980	Aspartic proteinase nepenthesin-2 precursor	AT2G39710
VIT_13s0019g01990	Phospholipid/glycerol acyltransferase	AT5G06090
VIT_13s0019g02000	PUMILIO 1 (APUM1)	AT2G29200
VIT_13s0019g02010	SRG1 (senescence-related gene 1)	AT3G21420
VIT_13s0019g02020	Thaumatin	AT5G02140
VIT_13s0019g02030	HAT dimerisation domain-containing protein	-
VIT_13s0019g02040	Lectin protein kinase	AT3G55550
VIT_13s0019g02050	Ribulose bisphosphate carboxylase/oxygenase activase, chloroplast	AT2G39730
VIT_13s0019g02060	Lateral organ boundaries domain protein 33 (LBD33)	AT5G06080
VIT_13s0019g02070	Phosphoribosylformylglycinamidine synthase, chloroplast precursor	-
VIT_13s0019g02080	DNA-binding protein	AT3G55560
VIT_13s0019g02090	Thylakoid lumenal 15 kDa protein 1	AT2G44920
VIT_13s0019g02100	No hit	-
VIT_13s0019g02110	fringe-related protein	AT2G37730
VIT_13s0019g02120	Zinc finger (C2H2 type) family	AT2G37740
VIT_13s0019g02130	Tropinone reductase	AT5G06060
VIT_13s0019g02140	Tropinone reductase	AT5G06060
VIT_13s0019g02150	Laccase	AT5G60020
VIT_13s0019g02160	Laccase	AT5G60020
VIT_13s0019g02170	Laccase	AT5G06060
VIT_13s0019g02180	Tropinone reductase	AT5G06060
VIT_13s0019g02190	No hit	-
VIT_13s0019g02200	Protein phosphatase 2CA AHG3 PP2CA	AT3G11410
VIT_13s0019g02210	Sterol 4-alpha-methyl-oxidase 1 (SMO1)	AT1G07420
VIT_13s0019g02220	No hit	-
VIT_13s0019g02230	PAP/25A associated domain containing protein	AT2G39740
VIT_13s0019g02240	Ribosomal protein S7 (RPS7B) 40S	AT3G02560
VIT_13s0019g02250	Ankyrin	AT2G39750
VIT_13s0019g02260	BTB-POZ and math Domain 3 ATBPM3	AT2G39760
VIT_13s0019g02270	Unknown protein	AT3G55570
VIT_13s0019g02280	Regulator of chromosome condensation (RCC1)	AT3G55580
VIT_13s0019g02290	Wall-associated receptor kinase-like 20	AT5G02070
VIT_13s0019g02300	Wall-associated receptor kinase-like 20	AT5G02070
VIT_13s0019g02310	Translation initiation factor eIF-3 subunit 4	AT3G11400
VIT_13s0019g02320	No hit	-
VIT_13s0019g02340	Unknown protein	AT3G53850
VIT_13s0019g02350	Glycoprotein, Mitochondrial	AT3G55605

VIT_13s0019g02360	Pyrroline-5-carboxylate synthetase	AT3G55610
VIT_13s0019g02370	Yip1 domain, member 2	AT2G39805
VIT_13s0019g02380	Exostosin	-
VIT_13s0019g02390	Dihydrofolate synthetase	AT5G05980
VIT_13s0019g02400	Transducin protein	AT5G05970
VIT_13s0019g02410	Serine/threonine protein phosphatase PP1	AT2G39840
VIT_13s0019g02430	LIM domain containing protein	AT2G39830
VIT_13s0019g02440	Mitochondrial substrate carrier family protein	AT3G53940
VIT_13s0019g02450	BEL1-like homeodomain protein 9 LSN (LARSON)	AT5G02030
VIT_13s0019g02460	Proton-dependent oligopeptide transport (POT) family protein	AT2G37900
VIT_13s0019g02470	RAB GTPase RABA2B	AT1G07410
VIT_13s0019g02480	Subtilisin serine endopeptidase (XSP1)	AT4G00230
VIT_13s0019g02490	Subtilisin protease C1	AT5G59190
VIT_13s0019g02500	No hit	-
VIT_13s0019g02510	CCR4-NOT transcription complex, subunit 4	-
VIT_13s0019g02520	Subtilisin protease C1	AT5G58830
VIT_13s0019g02530	Subtilisin protease C1	AT5G59190
VIT_13s0019g02540	Subtilisin protease C1	AT5G59190
VIT_13s0019g02550	Subtilisin protease C1	AT5G59100
VIT_13s0019g02560	Subtilisin protease C1	AT5G59100
VIT_13s0019g02580	Subtilisin protease C1	AT5G59100
VIT_13s0019g02590	Subtilisin protease C1	AT5G59190
VIT_13s0019g02600	Subtilisin protease C1	AT5G59120
VIT_13s0019g02610	Subtilisin protease C1	AT5G59190
VIT_13s0019g02620	Subtilisin protease C1	AT5G59190
VIT_13s0019g02630	Photosystem II PsbA	ATCG00020
VIT_13s0019g02640	Subtilisin protease C1	AT5G59190
VIT_13s0019g02650	U4/U6 small nuclear ribonucleoprotein SNU13	AT5G20160
VIT_13s0019g02660	Unknown protein	-
VIT_13s0019g02680	Unknown	-
VIT_13s0019g02690	Protease inhibitor/seed storage/lipid transfer protein (LTP)	AT3G53980
VIT_13s0019g02700	MEE60 (maternal effect embryo arrest 60)	AT5G05950
VIT_13s0019g02710	Rho guanyl-nucleotide exchange factor ROPGEF5	AT5G05940
VIT_13s0019g02720	Guanylyl cyclase (GC1)	AT5G05930
VIT_13s0019g02730	Unknown protein	AT3G54000
VIT_13s0019g02740	Heat shock protein 17.6 kDa class I	AT5G59720
VIT_13s0019g02750	No hit	-
VIT_13s0019g02760	Heat shock protein 17.6 kDa class I	AT5G59720
VIT_13s0019g02770	Heat shock protein 17.6 kDa class I	AT5G59720
VIT_13s0019g02780	Heat shock protein 17.6 kDa class I	AT5G59720

VIT_13s0019g02810	Glucuronosyl transferase	AT3G11340
VIT_13s0019g02820	Heat shock protein 18.2 kDa class I	AT5G59720
VIT_13s0019g02830	No hit	-
VIT_13s0019g02840	Heat shock protein 18.2 kDa class I	AT5G59720
VIT_13s0019g02850	Heat shock protein 17.6 kDa class I	AT5G59720
VIT_13s0019g02860	UDP-glucoronosyl and UDP-glucosyl transferase	AT3G55700
VIT_13s0019g02870	No hit	-
VIT_13s0019g02880	UDP-glucoronosyl/UDP-glucosyl transferase	AT3G11340
VIT_13s0019g02890	Glucosyltransferase-2	AT1G22360
VIT_13s0019g02900	Chaperone	AT1G53540
VIT_13s0019g02910	Cis-zeatin O-beta-D-glucosyltransferase	AT1G22400
VIT_13s0019g02920	Small heat-shock protein Cytosolic class I	-
VIT_13s0019g02930	Heat shock protein 17.6 kDa class I	-
VIT_13s0019g02940	Cis-zeatin O-beta-D-glucosyltransferase	AT1G22400
VIT_13s0019g02950	UGT76C2 (UDP-glucosyl transferase 76C2)	AT3G11340
VIT_13s0019g02960	UGT76C2 (UDP-glucosyl transferase 76C2)	AT3G11340
VIT_13s0019g02980	No hit	-
VIT_13s0019g02990	Cis-zeatin O-beta-D-glucosyltransferase	AT1G22360
VIT_13s0019g03000	Heat shock protein 17.6 kDa class I	-
VIT_13s0019g03010	Heat shock protein 17.6 kDa class I	-
VIT_13s0019g03020	Glucosyltransferase-2	AT1G22360
VIT_13s0019g03030	Chaperone	AT5G59720
VIT_13s0019g03040	Indole-3-acetate beta-glucosyltransferase	AT1G22360
VIT_13s0019g03050	Heat shock protein 17.6 kDa class I	-
VIT_13s0019g03060	Glucosyltransferase-2	AT1G22360
VIT_13s0019g03070	Heat shock protein 17.6 kDa class I	-
VIT_13s0019g03080	No hit	-
VIT_13s0019g03090	Heat shock protein class I (HSP17.8-CI)	-
VIT_13s0019g03100	Cis-zeatin O-beta-D-glucosyltransferase	AT1G22400
VIT_13s0019g03110	Heat shock protein 17.6 kDa class I	-
VIT_13s0019g03120	Glucosyltransferase-2	AT1G22400
VIT_13s0019g03130	Glucosyltransferase-2	AT1G22400
VIT_13s0019g03140	Heat shock protein 17.6 kDa class I	-
VIT_13s0019g03150	Membrane protein	-
VIT_13s0019g03160	Heat shock protein 17.6 kDa class I	-
VIT_13s0019g03170	Heat shock protein 16.9 kDa class I	AT3G46230
VIT_13s0019g03180	Unknown protein	AT5G05840
VIT_13s0019g03190	Zinc finger (C3HC4-type ring finger)	AT5G05830
VIT_13s0019g03200	Myb domain protein 109	AT3G55730
VIT_13s0019g03210	Lectin-like protein	AT5G01090

VIT_13s0019g03220	Proline transporter 1 (ProT1)	AT2G39890
VIT_13s0019g03230	Unknown protein	-
VIT_13s0019g03240	Syntaxin 18	AT1G51740
VIT_13s0019g03250	Auxin-independent growth promoter	AT2G37980
VIT_13s0019g03260	Ribosomal protein L35a (RPL35aC) 60S	AT1G07070
VIT_13s0019g03270	Phosphate translocator protein2, Plastidic	AT3G11320
VIT_13s0019g03280	LIM domain containing protein	AT3G55770
VIT_13s0019g03290	Unknown protein	AT2G39910
VIT_13s0019g03300	Glycosyl hydrolase family 17	-
VIT_13s0019g03310	Transposon protein	AT5G05800
VIT_13s0019g03320	Acid phosphatase class B	AT2G39920
VIT_13s0019g03330	Adenylosuccinate lyase	AT1G36280
VIT_13s0019g03340	No hit	-
VIT_13s0019g03350	Sedoheptulose-1,7-bisphosphatase (SBPase), Chloroplast	-
VIT_13s0019g03360	Laccase	-
VIT_13s0019g03370	Myb family	-
VIT_13s0019g03380	Coronatine-insensitive protein 1	AT2G39940
VIT_13s0019g03390	Unknown protein	AT2G39950
VIT_13s0019g03400	Signal peptidase complex subunit 2	AT2G39960
VIT_13s0019g03410	Peroxisomal membrane protein (PMP36)	AT2G39970
VIT_13s0019g03420	C2 domain-containing protein	AT1G07310
VIT_13s0019g03430	Anthocyanin 5-aromatic acyltransferase	AT2G39980
VIT_13s0019g03450	Unknown protein	AT3G55820
VIT_13s0019g03460	Homeodomain transcription factor 5	AT3G11260
VIT_13s0019g03470	Translation initiation factor eIF-3 subunit 5	AT2G39990
VIT_13s0019g03480	HAD superfamily hydrolase	AT3G45740
VIT_13s0019g03490	Zinc finger (CCCH-type) family protein	AT2G20280
VIT_13s0019g03510	Zinc finger (CCCH-type) family protein	AT2G20280
VIT_13s0019g03520	No hit	-
VIT_13s0019g03530	No hit	-
VIT_13s0019g03540	Regulator of nonsense transcripts 2 UPF2	AT2G39260
VIT_13s0019g03550	APETALA2 (AP2) floral homeotic protein	AT4G36920
VIT_13s0019g03560	Unknown protein	AT5G13610
VIT_13s0019g03570	Unknown protein	AT3G11760
VIT_13s0019g03580	Unknown	-
VIT_13s0019g03590	Catalytic	AT3G54970
VIT_13s0019g03600	Nuclear transcription factor Ysubunit B-8	AT2G37060
VIT_13s0019g03610	RNA recognition motif (RRM)-containing protein	AT3G54770
VIT_13s0019g03620	PWWP domain-containing protein	AT3G09670
VIT_13s0019g03630	Unknown	-

VIT_13s0019g03640	Ribosomal protein S23 (RPS23B) 40S	AT5G02960
VIT_13s0019g03650	RARE-cold-inducible 2A	AT2G38905
VIT_13s0019g03660	Unknown protein	AT5G51960
VIT_13s0019g03670	Unknown protein	AT5G63220
VIT_13s0019g03680	Unknown protein	AT2G35820
VIT_13s0019g03690	fertility restorer salt-inducible	AT2G16880
VIT_13s0019g03700	Lateral organ boundaries protein 1	AT1G07900
VIT_13s0019g03710	Lateral organ boundaries protein 1	AT1G07900
VIT_13s0019g03720	Lateral organ boundaries protein 11	AT2G28500
VIT_13s0019g03730	No hit	-
VIT_13s0019g03750	Lateral organ boundaries protein 11	AT2G28500
VIT_13s0019g03760	Lateral organ boundaries protein 11	AT2G28500
VIT_13s0019g03770	DNA-directed RNA polymerase subunit beta'	-
VIT_13s0019g03780	Lateral organ boundaries protein 11	AT2G28500
VIT_13s0019g03800	Lateral organ boundaries protein 1	AT1G07900
VIT_13s0019g03810	Lateral organ boundaries protein 1	AT1G07900
VIT_13s0019g03820	Lateral organ boundaries protein 11	AT2G28500
VIT_13s0019g03830	Lateral organ boundaries protein 11	AT2G28500
VIT_13s0019g03840	Lateral organ boundaries protein 1	AT1G07900
VIT_13s0019g03860	F-type H+-transporting ATPase d chain	AT3G52300
VIT_13s0019g03870	Substrate carrier, Mitochondrial	AT2G35800
VIT_13s0019g03880	DnaJ homolog, subfamily C, member 19	AT2G35795
VIT_13s0019g03890	Calmodulin binding protein	AT5G03040
VIT_13s0019g03910	Unknown	-
VIT_13s0019g03920	Elongation factor 1-alpha 1	AT5G60390
VIT_13s0019g03930	No hit	-
VIT_13s0019g03940	Unknown protein	AT2G35790
VIT_13s0019g03950	DNA-binding bromodomain-containing	AT2G34900
VIT_13s0019g03960	Alpha-taxilin	AT5G50840
VIT_13s0019g03970	Ribosomal protein P0 (RPP0A) acidic 60S	AT2G40010
VIT_13s0019g03980	Transcription initiation factor TFIIF beta subunit	AT3G52270
VIT_13s0019g03990	Unknown protein	AT4G25030
VIT_13s0019g04000	Pseudouridine synthase, RluA	AT3G52260
VIT_13s0019g04010	Myb family transcription factor	AT3G52250
VIT_13s0019g04020	CTP synthase	AT3G12670
VIT_13s0019g04030	Serine carboxypeptidase SCPL27	AT3G07990
VIT_13s0019g04040	Serine carboxypeptidase 28 (SCPL28)	AT2G35770
VIT_13s0019g04050	TET6 (tetraspanin6)	AT3G12090
VIT_13s0019g04060	MLO1	AT1G61560
VIT_13s0019g04070	MLO1	AT2G39200

VIT_13s0019g04080	Protein transport protein Sec61 subunit beta	AT5G60460
VIT_13s0019g04090	Ubiquitin-conjugating enzyme E2 C	AT1G50490
VIT_13s0019g04100	Zinc finger (C3HC4-type ring finger)	AT2G37150
VIT_13s0019g04110	Retrotransposon protein	-
VIT_13s0019g04120	Rhomboid	AT3G07950
VIT_13s0019g04130	AarF domain containing kinase	AT2G39190
VIT_13s0019g04140	LHCA1	AT3G54890
VIT_13s0019g04150	Receptor protein kinase CRINKLY4 precursor	AT2G39180
VIT_13s0019g04160	Protein kinase	AT1G16670
VIT_13s0019g04170	Para-aminobenzoate (PABA) synthase	AT2G28880
VIT_13s0019g04180	Aminodeoxychorismate synthase/glutamine amidotransferase	AT2G28880
VIT_13s0019g04190	Chorismate synthase 1, chloroplast precursor	AT1G48850
VIT_13s0019g04200	Patatin	AT3G54950
VIT_13s0019g04210	No hit	-
VIT_13s0019g04220	Tryptophan/tyrosine permease family	AT5G19500
VIT_13s0019g04230	V-type H+-transporting ATPase subunit G	AT3G01390
VIT_13s0019g04240	Protein disulfide-isomerase A1	AT5G60640
VIT_13s0019g04250	Unknown protein	AT5G14990
VIT_13s0019g04260	Monoglyceride lipase	AT5G19290
VIT_13s0019g04270	No hit	-
VIT_13s0019g04280	Aquaporin PIP2B	AT2G37170
VIT_13s0019g04290	No hit	-
VIT_13s0019g04300	Ribosomal protein L12 (RPL12A) 60S	AT2G37190
VIT_13s0019g04310	DCP2 (decapping 2)	AT5G13570
VIT_17s0000g05170	No hit	-
VIT_17s0000g05180	Unknown	-
VIT_17s0000g05190	Unknown protein	AT3G26850
VIT_17s0000g05200	NLI interacting factor (NIF) family protein	AT3G29760
VIT_17s0000g05210	LNG1 (LONGIFOLIA1)	AT1G74160
VIT_17s0000g05220	TCP family transcription factor TCP5	AT5G60970
VIT_17s0000g05230	Unknown protein	AT5G08060
VIT_17s0000g05240	Nuclear transport factor 2 (NTF2)	AT5G60980
VIT_17s0000g05250	Unknown protein	AT5G08050
VIT_17s0000g05260	Unknown protein	-
VIT_17s0000g05270	Unknown protein	AT4G14840
VIT_17s0000g05280	UPF0737 protein AFP3	-
VIT_17s0000g05290	Pre-mRNA cleavage complex II protein Clp1	AT5G11010
VIT_17s0000g05300	Pre-mRNA cleavage complex II protein Clp1	AT5G11010
VIT_17s0000g05310	Pre-mRNA cleavage complex II protein Clp1	AT5G11010
VIT_17s0000g05320	IFA binding protein	AT1G74830

VIT_17s0000g05330	Serine/threonine protein phosphatase PP2A-5 catalytic subunit (PP2A5)	AT1G10430
VIT_17s0000g05350	5-formyltetrahydrofolate cycloligase	AT5G13050
VIT_17s0000g05360	Germin	AT1G18980
VIT_17s0000g05370	MYC ZCW32 (bigpetal, bigpetalub)	AT5G62610
VIT_17s0000g05380	Dynein light chain LC8-type	AT5G20110
VIT_17s0000g05390	Unknown protein	AT3G47850
VIT_17s0000g05400	Myb domain protein 35	AT3G28470
VIT_17s0000g05410	Galactosyltransferase	AT1G74800
VIT_17s0000g05420	AAA-type ATPase family	AT3G28510
VIT_17s0000g05430	Aminoacyl-tRNA synthetase	AT1G18950
VIT_17s0000g05440	Unknown protein	AT1G74790
VIT_17s0000g05450	ELF5 (early flowering 5)	AT5G62640
VIT_17s0000g05460	Nodulin	AT1G74780
VIT_17s0000g05470	Nodulin	AT1G74780
VIT_17s0000g05480	EMB2454 (embryo defective 2454)	AT1G18920
VIT_17s0000g05490	Lateral organ boundaries domain family protein (LBD27)	AT3G47870
VIT_17s0000g05500	Cysteine endopeptidase	AT3G47910
VIT_17s0000g05510	Pentatricopeptide (PPR) repeat-containing protein	AT1G74750
VIT_17s0000g05520	Calcium-dependent protein kinase 30 CPK30	AT1G18890
VIT_17s0000g05530	DnaJ homolog, subfamily B, member 4	AT3G47940
VIT_17s0000g05540	H (+)-ATPase 11 AHA11	AT5G62670
VIT_17s0000g05550	Proton-dependent oligopeptide transport (POT) family protein	AT5G62680
VIT_17s0000g05560	Proton-dependent oligopeptide transport (POT) family protein	AT5G28470
VIT_17s0000g05570	Receptor protein kinase	AT5G62710
VIT_17s0000g05580	Isopiperitenol dehydrogenase	AT2G47140
VIT_17s0000g05600	(-)-isopiperitenol dehydrogenase	AT2G47140
VIT_17s0000g05610	Isopiperitenol dehydrogenase	AT2G47140
VIT_17s0000g05620	Integral membrane HPP family protein	AT5G62720
VIT_17s0000g05630	Homeodomain leucine zipper protein HB-1	AT3G01470
VIT_17s0000g05640	Nitrate transporter 1:2	AT1G69850
VIT_17s0000g05650	Unknown protein	AT1G74730
VIT_17s0000g05660	Polygalacturonase GH28	AT1G23460
VIT_17s0000g05670	Polygalacturonase GH28	AT3G15720
VIT_17s0000g05680	Band 7 family	AT5G62740
VIT_17s0000g05690	Isochorismate synthase 1, chloroplast precursor	AT3G01280
VIT_17s0000g05700	Phosphoribosylanthranilate transferase	AT1G74720
VIT_17s0000g05710	Unknown	-
VIT_17s0000g05720	No hit	-
VIT_17s0000g05730	No hit	-
VIT_17s0000g05740	Pectate lyase, N-terminal	AT3G01270

VIT_17s0000g05750	Isochorismate synthase (ICS1/SID2) (ICS2)	AT1G18870
VIT_17s0000g05760	Nuclear protein ZAP	AT5G62760
VIT_17s0000g05770	Nuclear ribonuclease Z	AT1G74700
VIT_17s0000g05780	Unknown protein	AT1G18850
VIT_17s0000g05790	Cupin, RmlC-type	AT5G39890
VIT_17s0000g05800	Delta-1-pyrroline-5-carboxylate dehydrogenase (P5CDH)	AT5G62530
VIT_17s0000g05810	WRKY DNA-binding protein 72	AT5G15130
VIT_17s0000g05820	Ubiquitin-conjugating enzyme E2 A	AT2G02760
VIT_17s0000g05830	Unknown protein	AT5G62550
VIT_17s0000g05840	Calmodulin binding IQD31 (IQ-domain 31)	AT1G74690
VIT_17s0000g05850	ATATH1 (ABC2 homolog1)	AT3G47730
VIT_17s0000g05860	ATATH6 (ABC2 homolog 6)	AT3G47780
VIT_17s0000g05870	Aldose 1-epimerase protein	AT3G47800
VIT_17s0000g05880	Calcineurin phosphoesterase	AT3G47810
VIT_17s0000g05890	Protein kinase APK1B	AT2G02800
VIT_17s0000g05900	Basic helix-loop-helix (bHLH) family	AT1G74500
VIT_17s0000g05910	No hit	-
VIT_17s0000g05920	Kelch repeat-containing F-box protein	AT1G74510
VIT_17s0000g05930	No hit	-
VIT_17s0000g05940	Chromosome structural maintenance protein MAG2	AT3G47700
VIT_17s0000g05950	PRE1 (Paclobutrazol resistance1)	AT3G28857
VIT_17s0000g05960	Pectinesterase family	-
VIT_17s0000g05970	Ribosomal protein S9 (RPS9C) 40S	AT5G39850
VIT_17s0000g05980	Zinc finger protein / regulator of chromosome condensation (RCC1)	AT5G19420
VIT_17s0000g05990	ABA-responsive protein (HVA22a)	AT1G74520
VIT_17s0000g06000	Basic helix-loop-helix (bHLH) family	AT3G47640
VIT_17s0000g06010	Unknown protein	AT1G74530
VIT_17s0000g06020	TCP family transcription factor TCP14	AT3G47620
VIT_17s0000g06030	Nucleosome assembly protein (NAP-related) NRP2	AT1G74560
VIT_17s0000g06040	Phytochrome kinase substrate 1	AT1G18810
VIT_17s0000g06050	Ankyrin protein kinase	AT1G26850
VIT_17s0000g06060	Transcription regulator/ zinc ion binding	AT3G47610
VIT_17s0000g06070	No hit	-
VIT_17s0000g06080	No hit	-
VIT_17s0000g06090	Pentatricopeptide (PPR) repeat-containing protein	AT1G74580
VIT_17s0000g06100	Pentatricopeptide (PPR) repeat-containing protein	AT1G74600
VIT_17s0000g06110	Glutathione S-transferase 9 GSTU9	AT5G62480
VIT_17s0000g06120	Glutathione S-transferase 9 GSTU9	AT5G62480
VIT_17s0000g06130	Glutathione S-transferase 9 GSTU9	AT5G62480
VIT_17s0000g06140	Glutathione S-transferase 9 GSTU9	AT5G62480

VIT_17s0000g06150	Glutathione S-transferase 9 GSTU9	AT5G62480
VIT_17s0000g06170	Pentatricopeptide (PPR) repeat-containing	AT1G74630
VIT_17s0000g06180	Hydrolase, alpha/beta fold	AT1G74640
VIT_17s0000g06190	Myb domain protein 94	AT1G74650
VIT_17s0000g06200	Mini zinc finger 1 MIF1	AT1G74660
VIT_17s0000g06210	GASA like	AT1G74670
VIT_17s0000g06220	Exostosin	AT1G74680
VIT_17s0000g06230	Zinc finger (C3HC4-type ring finger)	AT5G62460
VIT_17s0000g06240	Unknown protein	AT5G62440
VIT_17s0000g06250	RWP-RK domain-containing protein	AT1G18790
VIT_17s0000g06260	Pentatricopeptide (PPR) repeat-containing protein	AT3G47530
VIT_17s0000g06270	Malate dehydrogenase precursor	AT3G47520
VIT_17s0000g06280	Geranylgeranyl reductase	AT1G74470
VIT_17s0000g06290	Lipase GDSL	AT1G74460
VIT_17s0000g06300	No hit	-
VIT_17s0000g06310	Cycling DOF factor 2	AT3G47500
VIT_17s0000g06320	Endonuclease	AT3G47490
VIT_17s0000g06330	Lipoate protein ligase	AT3G29010
VIT_17s0000g06340	MADS-box agamous-like 30	AT1G18750
VIT_17s0000g06350	LHCA4 (Photosystem I light harvesting complex gene 4)	AT3G47470
VIT_17s0000g06360	Alpha-expansin 3	AT1G69530
VIT_17s0000g06370	Thioredoxin 2	AT1G08570
VIT_17s0000g06380	YGL010w	AT1G18720
VIT_17s0000g06390	Pentatricopeptide (PPR) repeat-containing protein	AT1G59720
VIT_17s0000g06400	NAC domain containing protein 100	AT5G61430
VIT_17s0000g06410	MYB transcription factor MIXTA-like 2	AT3G01140
VIT_17s0000g06420	Galactosyl transferase GMA12/MNN10	AT1G18700
VIT_17s0000g06430	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	AT1G26550
VIT_17s0000g06440	Galactoside 2-alpha-L-fucosyltransferase	AT2G03220
VIT_17s0000g06450	Ribulose-phosphate 3-epimerase, chloroplast precursor	AT5G61410
VIT_17s0000g06460	Zinc finger (C3HC4-type ring finger)	AT1G74410
VIT_17s0000g06470	Pentatricopeptide (PPR) repeat-containing protein	AT5G61400
VIT_17s0000g06480	Pentatricopeptide (PPR) repeat-containing protein	-
VIT_17s0000g06490	MKK5	-
VIT_17s0000g06500	Pentatricopeptide (PPR) repeat-containing	AT5G66520
VIT_17s0000g06510	Exonuclease	AT5G61390
VIT_17s0000g06520	Timing of CAB expression 1	AT5G61380
VIT_17s0000g06530	No hit	-
VIT_17s0000g06540	Exonuclease	-
VIT_17s0000g06550	Exonuclease	-

VIT_17s0000g06560	Retrovirus Pol polyprotein from transposon TNT 1-94	AT3G29785
VIT_17s0000g06570	Timing of CAB expression 1 protein	AT5G61380
VIT_17s0000g06580	Vesicle transport v-SNARE 11	AT5G39510
VIT_17s0000g06590	Galactosyl transferase GMA12/MNN10	AT1G74380
VIT_17s0000g06600	No hit	-
VIT_17s0000g06610	Zinc finger (C3HC4-type ring finger)	AT1G18660
VIT_17s0000g06620	Protein kinase pto	AT5G61350
VIT_17s0000g06630	Unknown protein	AT5G61340
VIT_17s0000g06640	formin-2	AT2G25050
VIT_17s0000g06650	IBS1 (impaired in baba-induced sterility 1)	AT1G18670
VIT_17s0000g06660	HNH endonuclease domain-containing protein	AT1G18680
VIT_17s0000g06670	Translation initiation factor eIF-5A	AT1G13950
VIT_17s0000g06680	Unknown protein	AT2G03350
VIT_17s0000g06690	Unknown	-
VIT_17s0000g06700	No hit	-
VIT_17s0000g06710	Leucine-rich repeat transmembrane protein kinase	AT1G74360
VIT_17s0000g06720	No hit	-
VIT_17s0000g06730	No hit	-
VIT_17s0000g06740	Zinc finger (C2H2 type) family	-
VIT_17s0000g06750	Unknown protein	AT3G25400
VIT_17s0000g06760	Unknown protein	AT1G69360
VIT_17s0000g06770	Pentatricopeptide (PPR) repeat-containing protein	AT2G02980
VIT_17s0000g06780	Dimethylaniline monooxygenase	AT5G07800
VIT_17s0000g06790	flavin-containing monooxygenase	AT5G07800
VIT_17s0000g06800	Unknown protein	-
VIT_17s0000g06810	Myb family transcription factor / ELM2 domain-containing	AT1G26580
VIT_17s0000g06820	Zinc finger (C2H2 type) family	AT1G26610
VIT_17s0000g06830	Zinc finger (C2H2 type) family	-
VIT_17s0000g06840	Unknown protein	AT5G07890
VIT_17s0000g06850	No hit	-
VIT_17s0000g06860	SNAP25ous protein SNAP30	AT5G61210
VIT_17s0000g06870	Oxidoreductase, acting on NADH or NADPH	AT5G61220
VIT_17s0000g06880	Heparanase protein 2 precursor	AT5G07830
VIT_17s0000g06890	Unknown protein	-
VIT_17s0000g06900	DNA helicase SNF2 domain-containing protein	AT5G07810
VIT_17s0000g06920	Remorin	-
VIT_17s0000g06930	Unfertilized embryo sac 10 UNE10	AT4G00050
VIT_17s0000g06940	LAP4 protein	AT5G07910
VIT_17s0000g06950	DEAH (Asp-Glu-Ala-His) box polypeptide 16	AT1G32490
VIT_17s0000g06960	UDP-glucose 6-dehydrogenase	AT5G15490

VIT_17s0000g06970	Diacylglycerol kinase 1	AT5G07920
VIT_17s0000g06980	Ribosomal protein S19 (RPS19C) 40S	AT5G61170
VIT_17s0000g06990	Ribosomal protein L2	ATCG01310
VIT_17s0000g07000	VIP4	AT5G61150
VIT_17s0000g07010	5-azacytidine resistance	-
VIT_17s0000g07020	Cis-zeatin O-beta-D-glucosyltransferase	AT3G02100
VIT_17s0000g07030	Cis-zeatin O-beta-D-glucosyltransferase	AT3G02100
VIT_17s0000g07060	UDP-glucosyltransferase HRA25	AT3G02100
VIT_17s0000g07070	UDP-glucoronosyl and UDP-glucosyl transferase	AT3G02100
VIT_17s0000g07080	UDP-glucosyltransferase HRA25	AT3G02100
VIT_17s0000g07090	UDP-glucoronosyl and UDP-glucosyl transferase	AT3G02100
VIT_17s0000g07100	UDP-glucosyltransferase HRA25	AT3G02100
VIT_17s0000g07120	Unknown protein	AT5G07960
VIT_17s0000g07130	Unknown protein	AT5G07950
VIT_17s0000g07140	Unknown protein	AT5G07950

F_{ST} Wine &Table		
Gene stable ID	**Functional annotation**	**Arabidopsis homolog**
VIT_01s0011g00010	Transcription initiation factor IIE (TFIIE) alpha subunit	AT1G03280
VIT_01s0011g00030	ACT domain containing protein (ACR4)	AT1G69040
VIT_01s0011g00040	No hit	-
VIT_01s0011g00050	Heat shock protein binding	AT1G69060
VIT_01s0011g00060	No hit	-
VIT_01s0011g00070	Nucleolar complex protein 14 nop14	AT1G69070
VIT_01s0011g00080	Universal stress protein (USP) family protein	AT2G03720
VIT_01s0011g00090	Zinc finger (C3HC4-type ring finger)	AT5G15790
VIT_01s0011g00100	MADS-box APETALA 1	AT1G69120
VIT_01s0011g00110	SEPALLATA1	AT5G15800
VIT_01s0011g00120	Unknown protein	AT1G69160
VIT_01s0011g00130	Squamosa promoter-binding protein 6 (SPL6)	AT1G69170
VIT_01s0011g00140	CRABS CLAW	AT1G69180
VIT_01s0011g00150	Unknown protein	AT1G26330
VIT_01s0011g00160	Alpha-1,4-glucan-protein synthase	AT3G08900
VIT_01s0011g00170	Brassinosteroid-6-oxidase [Vitis vinifera]	AT5G38970
VIT_01s0011g00190	Brassinosteroid-6-oxidase [Vitis vinifera]	AT3G30180
VIT_01s0011g00210	Cytochrome b5 isoform Cb5-D	AT1G26340
VIT_01s0011g00230	Dihydropterin pyrophosphokinase /dihydropteroate synthase	AT4G30000
VIT_01s0011g00240	Fructokinase-2	AT1G69200
VIT_01s0011g00250	6-phosphogluconolactonase	AT1G13700
VIT_01s0011g00280	feronia receptor-like kinase	AT3G51550
VIT_01s0011g00290	Unknown protein	AT1G69210
VIT_01s0011g00300	SIK1 (serine/threonine kinase 1)	AT1G69220
VIT_01s0011g00340	Glycosyl hydrolase family 28 protein	AT1G78400
VIT_01s0011g00350	CYP78A5	AT1G13710
VIT_01s0011g00370	SP1L2 (SPIRAL2)	-
VIT_01s0011g00380	SP1L1 (SPIRAL1-like1)	AT3G29770
VIT_01s0011g00390	Asparagine synthase	AT2G03667
VIT_01s0011g00400	Nuclear transport factor 2 (NTF2)	AT5G60980
VIT_01s0011g00410	Nuclear transport factor 2 (NTF2)	AT1G13740
VIT_01s0011g00420	RPK1 (receptor-like protein kinase 1)	AT3G02130
VIT_01s0011g00440	Unknown	-
VIT_01s0011g00450	Magnesium transporter CorA	AT2G03620
VIT_01s0011g00460	Unknown protein	AT5G61040
VIT_01s0011g00470	Metallophosphatase	AT1G13750
VIT_01s0011g00490	Pentatricopeptide (PPR) repeat-containing protein	AT1G69290

VIT_01s0011g00500	RUS1 (Root uvb sensitive 1)	AT1G13770
VIT_01s0011g00510	Unknown protein	AT1G26750
VIT_01s0011g00520	Pentatricopeptide (PPR) repeat-containing	AT1G26500
VIT_01s0011g00530	Ureide permease 2 (AtUPS2)	AT2G03530
VIT_01s0011g00540	SPFH domain-containing protein 2 precursor band 7 family	AT2G03510
VIT_01s0011g00550	Hydrolase, alpha/beta fold family	AT1G13820
VIT_01s0011g00570	Glucan endo-1,3-beta-glucosidase 3 precursor	-
VIT_01s0011g00580	Pentatricopeptide (PPR) repeat-containing protein	AT1G26460
VIT_01s0011g00590	Acclimation of photosynthesis to environment	AT5G46110
VIT_01s0011g00600	Acclimation of photosynthesis to environment	AT5G46110
VIT_01s0011g00610	Unknown protein	AT1G26470
VIT_04s0008g04590	CXE carboxylesterase	AT3G27320
VIT_04s0008g04600	Expansin family protein (EXPR3)	-
VIT_04s0008g04610	PDE247 (pigment defective 247)	AT2G20540
VIT_04s0008g04620	Expansin family protein (EXPR3)	-
VIT_04s0008g04630	Pentatricopeptide repeat-containing protein	AT2G20540
VIT_04s0008g04640	Pentatricopeptide repeat-containing protein	AT2G20540
VIT_04s0008g04670	Blight-associated protein p12 precursor	-
VIT_04s0008g04680	No hit	-
VIT_04s0008g04690	Proteasome 26S AAA-ATPase subunit (RPT6a)	AT5G19990
VIT_04s0008g04700	Histone H2A variant 3 HTA9	AT1G52740
VIT_04s0008g04710	Beta-ketoacyl-CoA synthase	AT2G26640
VIT_04s0008g04720	Endonuclease/exonuclease/phosphatase family protein	AT5G11350
VIT_04s0008g04730	Unknown protein	AT2G25605
VIT_04s0008g04740	GCN5 N-acetyltransferase (GNAT)	AT5G11340
VIT_04s0008g04750	Monooxygenase	AT5G11330
VIT_04s0008g04760	V-type H+-transporting ATPase 21kDa proteolipid subunit	AT4G32530
VIT_04s0008g04770	Zinc finger protein VAR3, chloroplastic	-
VIT_04s0008g04780	Protein phosphatase 2C DBP	AT2G25620
VIT_04s0008g04790	ABC transporter g family pleiotropic drug resistance 12 PDR12	AT1G15520
VIT_04s0008g04800	Transferase	AT4G29250
VIT_04s0008g04810	Unknown	ATCG00480
VIT_04s0008g04820	ABC transporter g family pleiotropic drug resistance 12 PDR12	AT1G15520
VIT_04s0008g04830	ABC transporter g family pleiotropic drug resistance 12 PDR12	AT1G15520
VIT_04s0008g04840	ABC transporter g family pleiotropic drug resistance 12 PDR12	AT4G00980
VIT_04s0008g04860	No hit	-
VIT_04s0008g04870	flavin monooxygenase-like protein	AT5G11320
VIT_04s0008g04880	Indole-3-acetic acid-amido synthetase GH3.1	-
VIT_04s0008g04890	WD-40 repeat protein (LEUNIG)	AT4G32551
VIT_04s0008g04900	WD-40 repeat protein (LEUNIG)	AT4G32551

VIT_04s0008g04910	WD-40 repeat protein (LEUNIG)	AT4G32551
VIT_04s0008g04920	2-oxoglutarate-dependent dioxygenase	AT1G52820
VIT_04s0008g04930	Paramyosin	AT4G32560
VIT_04s0008g04940	Gibberellin 3beta-hydroxylase3	AT1G15550
VIT_04s0008g04950	TIFY 8	AT4G32570
VIT_04s0008g04960	Pentatricopeptide (PPR) repeat-containing protein	AT5G11310
VIT_04s0008g04970	1-deoxy-D-xylulose-5-phosphate synthase, chloroplast precursor	AT5G11380
VIT_04s0008g04980	Boron transporter-like protein 4	AT1G15460
VIT_04s0008g04990	Potassium channel AKT1	AT2G26650
VIT_04s0008g05000	Ubiquinol-cytochrome c reductase subunit 7	AT4G32470
VIT_04s0008g05010	Unknown protein	AT5G11420
VIT_04s0008g05020	Ras GTP-binding protein (RAN3)	AT5G20020
VIT_04s0008g05030	Ras GTP-binding protein (RAN3)	AT5G55190
VIT_04s0008g05040	Agenet domain-containing protein	AT4G32440
VIT_04s0008g05050	Pentatricopeptide (PPR) repeat-containing protein	AT3G54980
VIT_04s0008g05060	C-5 cytosine-specific DNA methylase	AT5G25480
VIT_04s0008g05070	Pentatricopeptide (PPR) repeat-containing	AT2G25580
VIT_04s0008g05080	Ammonium transporter 2	AT2G38290
VIT_04s0008g05090	Peptidyl-prolyl isomerase D (cyclophilin D)	AT4G32420
VIT_04s0008g05100	Cytochrome c oxidase subunit Vb	AT3G15640
VIT_04s0008g05110	Unknown	-
VIT_04s0008g05120	Phospholipase/carboxylesterase	AT5G20060
VIT_04s0008g05130	TSO1 (chinese for 'ugly')	AT3G22780
VIT_04s0008g05140	TSO1 (chinese for 'ugly')	AT3G22780
VIT_04s0008g05150	Zinc finger (Ran-binding)	AT3G15680
VIT_04s0008g05160	Unknown protein	AT4G31980
VIT_04s0008g05170	Unknown protein	AT4G31980
VIT_04s0008g05180	Ankyrin	AT5G11280
VIT_04s0008g05190	Overexpressor of cationic peroxidase 3 (OCP3)	AT5G11270
VIT_04s0008g05200	No hit	-
VIT_04s0008g05210	BZIP protein HY5 (HY5)	AT5G11260
VIT_04s0008g05220	Cellulose synthase CESA1	AT4G32410
VIT_04s0008g05240	Brittle 1 protein	AT4G32400
VIT_04s0008g05250	Expansin family protein (EXPR3)	AT2G18660
VIT_04s0008g05260	Unknown	-
VIT_04s0008g05270	ATPase AFG1	AT2G25530
VIT_04s0008g05280	CRR2 (chlororespiratory reduction 2)	AT4G21065
VIT_04s0008g05290	No hit	-
VIT_04s0008g05300	Phosphate translocator	AT4G32390
VIT_04s0008g05310	Nod-factor receptor 1b	AT1G51940

VIT_04s0008g05320	Concanavalin A lectin	AT5G10530
VIT_04s0008g05330	DEAD box RNA helicase RH15	AT5G11200
VIT_04s0008g05340	Bundle-sheath defective protein 2	AT3G47650
VIT_04s0008g05350	Serine hydrolase [Vitis vinifera]	AT5G16080
VIT_04s0008g05360	Serine hydrolase [Vitis vinifera]	AT5G16080
VIT_04s0008g05370	Serine hydrolase [Vitis vinifera]	AT5G16080
VIT_04s0008g05380	Serine hydrolase [Vitis vinifera]	AT5G16080
VIT_04s0008g05390	Carboxyesterase17 CXE17	AT5G16080
VIT_04s0008g05400	Serine hydrolase [Vitis vinifera]	AT5G16080
VIT_04s0008g05410	Serine hydrolase [Vitis vinifera]	AT5G16080
VIT_04s0008g05420	SPX2 (SYG1/Pho81/XPR1) domain-containing protein SPX2	AT2G26660
VIT_04s0008g05430	RDR6 (RNA-dependent RNA polymerase 6)	AT3G49500
VIT_04s0008g05440	Ethylene-responsive transcription factor SHINE 3	AT5G11190
VIT_04s0008g05450	Phospholipase D alpha 1 precursor (PLD 1) (Choline phosphatase 1)	AT3G15730
VIT_04s0008g05460	Unknown protein	AT5G25360
VIT_04s0008g05470	EIN3-binding F-box protein 2	AT2G25490
VIT_04s0008g05480	BRI1-KD interacting protein 118	AT4G32330
VIT_04s0008g05490	L-ascorbate peroxidase.	AT4G32320
VIT_04s0008g05500	S-receptor kinase	AT4G32300
VIT_04s0008g05510	SYNC1 protein, related	AT3G11760
VIT_04s0008g05520	Unknown protein	AT3G24150
VIT_04s0008g05530	Unknown protein	AT4G32290
VIT_04s0008g05540	Clathrin assembly protein 2	AT2G25430
VIT_04s0008g05550	SHR5-receptor-like kinase	AT1G56130
VIT_04s0008g05560	IAA29	AT4G32280
VIT_04s0008g05570	UDP-glucuronic acid/UDP-N-acetylgalactosamine transporter	AT4G32272
VIT_04s0008g05580	Unknown protein	AT4G32270
VIT_04s0008g05590	F-type H+-transporting ATPase b chain CfoII	AT4G32260
VIT_04s0008g05600	KEG (keep on going)	AT4G32250
VIT_04s0008g05610	Centromeric protein	AT4G32190
VIT_04s0008g05620	Adenine phosphoribosyltransferase	AT5G11160
VIT_04s0008g05630	Phox	AT2G25350
VIT_04s0008g05640	Protease inhibitor/seed storage/lipid transfer protein (LTP)	AT4G12510
VIT_04s0008g05650	Vesicle-associated membrane protein 7	AT4G32150
VIT_04s0008g05670	FAR1-related sequence 6	AT1G52520
VIT_04s0008g05680	No hit	-
VIT_04s0008g05690	Meprin and TRAFy domain-containing protein	AT2G25320
VIT_04s0044g01000	Pectinesterase family	AT5G09760
VIT_04s0044g01010	Pectinesterase family	AT5G09760
VIT_04s0044g01020	Pectinesterase family	AT5G09760

VIT_04s0044g01030	Pectinesterase family	AT5G09760
VIT_04s0044g01040	Basic helix-loop-helix (bHLH) family	-
VIT_04s0044g01060	Leaf senescence related protein-like	AT1G48880
VIT_04s0044g01070	Leaf senescence related protein-like	AT1G48880
VIT_04s0044g01080	Pentatricopeptide (PPR) repeat	AT5G04780
VIT_04s0044g01090	Chromatin assembly factor-2 (FASCIATA2) (FAS2)	AT5G64630
VIT_04s0044g01100	Invertase/pectin methylesterase inhibitor	AT5G64620
VIT_04s0044g01110	Alcohol dehydrogenase 6	AT1G77120
VIT_04s0044g01120	Alcohol dehydrogenase 2 [Vitis vinifera]	AT1G77120
VIT_04s0044g01130	Alcohol dehydrogenase 2 [Vitis vinifera]	AT1G77120
VIT_04s0044g01140	RNA-binding protein Y14	AT1G51510
VIT_04s0044g01150	Aminotransferase, class V	-
VIT_04s0044g01160	Aminotransferase, class V	-
VIT_04s0044g01170	Aminotransferase, class V	-
VIT_04s0044g01180	Cell division protease FtsH	AT5G64580
VIT_04s0044g01190	Maternal effect embryo arrest 50	AT4G00231
VIT_04s0044g01200	Auxin-independent growth promoter	AT5G64600
VIT_04s0044g01210	Phosphatidylinositol 4-kinase	AT5G64070
VIT_04s0044g01220	NAC domain containing protein 103	AT5G64060
VIT_04s0044g01230	Unknown	-
VIT_04s0044g01240	PRLI-interacting factor G	AT2G13690
VIT_04s0044g01250	No hit	-
VIT_04s0044g01260	SEU3B protein	AT1G43850
VIT_04s0044g01270	Calcineurin phosphoesterase	AT1G48120
VIT_04s0044g01280	Beta-1,3-glucan synthase	AT2G13680
VIT_04s0044g01290	MAP3Ka	AT1G53570
VIT_04s0044g01300	DNA cross-link repair protein	AT1G19025
VIT_04s0044g01310	NADH-plastoquinone oxidoreductase subunit o	AT1G74880
VIT_04s0044g01320	ABCNAP13	AT4G33460
VIT_04s0044g01330	GDP-mannose transporter (GONST1)	AT2G13650
VIT_04s0044g01360	Unknown protein	AT5G09310
VIT_04s0044g01370	SCL1 (scarecrow-like 1)	AT1G21450
VIT_04s0044g01380	Myb domain protein 52	AT1G73410
VIT_04s0044g01410	Photosystem I reaction center subunit N (PSAN)	AT5G64040
VIT_04s0044g01420	Polygalacturonase GH28	AT4G33440
VIT_04s0044g01430	Unknown protein	AT1G31130
VIT_04s0044g01450	Unknown protein	-
VIT_04s0044g01460	PUB26 (plant U- box 26)	-
VIT_04s0044g01470	Cation/hydrogen exchanger (CHX15)	AT2G13620
VIT_04s0044g01480	3'(2'),5'-bisphosphate nucleotidase	AT5G63980

VIT_04s0044g01490	2-oxoisovalerate dehydrogenase alpha subunit, mitochondrial precursor	AT5G09300
VIT_04s0044g01500	NAC domain containing protein 104	AT5G64530
VIT_04s0044g01510	Histone deacetylase HDA14	AT4G33470
VIT_04s0044g01520	GA 20-oxidase 2	AT5G07200
VIT_04s0044g01530	UDP-glucuronic acid: anthocyanin glucuronosyltransferase	AT5G65550
VIT_04s0044g01540	UDP-glucuronic acid: anthocyanin glucuronosyltransferase	AT5G65550
VIT_04s0044g01550	Pentatricopeptide repeat	AT1G52640
VIT_04s0044g01560	Protein kinase	AT1G77280
VIT_04s0044g01570	DNA topoisomerase III alpha	AT5G63920
VIT_06s0080g00210	Histone deacetylase protein (HDA8)	AT1G08460
VIT_06s0080g00220	No hit	-
VIT_06s0080g00230	Unknown protein	AT2G27590
VIT_06s0080g00240	DTDP-glucose 4-6-dehydratase	AT1G08200
VIT_06s0080g00250	Sialyltransferase	AT1G08280
VIT_06s0080g00260	Seed maturation protein PM38	AT5G22470
VIT_06s0080g00270	Zinc finger (C2H2 type) protein (WIP3)	AT1G08290
VIT_06s0080g00280	Bile acid sodium symporter	AT3G56160
VIT_06s0080g00290	TFL1 (Terminal flower 1)	AT2G27550
VIT_06s0080g00300	Pentatricopeptide (PPR) repeat-containing	AT5G48910
VIT_06s0080g00310	Esterase/lipase/thioesterase family protein	AT5G22460
VIT_06s0080g00320	Esterase/lipase/thioesterase	AT5G22460
VIT_06s0080g00330	Esterase/lipase/thioesterase family protein	AT1G08310
VIT_06s0080g00340	ABI5 (ABA insensitive 5)	AT3G44460
VIT_06s0080g00350	Myo-inositol-1-phosphate synthase	AT5G22450
VIT_06s0080g00360	BZIP transcription factor	AT1G08320
VIT_06s0080g00370	F-box domain containing protein	AT1G67190
VIT_06s0080g00390	Endomembrane protein 70 protein	AT1G08350
VIT_06s0080g00400	Ribosomal protein L10A (RPL10aA) 60S	AT1G08360
VIT_06s0080g00410	ferredoxin	AT2G27510
VIT_06s0080g00420	Glucan endo-1,3-beta-glucosidase 7 precursor	AT2G27500
VIT_06s0080g00430	No hit	-
VIT_06s0080g00440	Ribosomal protein S9	AT3G49080
VIT_06s0080g00450	Calcium-binding protein CML	AT2G27480
VIT_06s0080g00460	Nuclear transcription factor Ysubunit B related	AT2G27470
VIT_06s0080g00470	RNA-binding region RNP-1	AT3G52660
VIT_06s0080g00500	Unknown	-
VIT_06s0080g00510	Sec23/sec24 transport family	AT2G27460
VIT_06s0080g00530	Aspartyl-tRNA synthetase	AT5G56680
VIT_06s0080g00540	Unknown protein	-
VIT_06s0080g00550	EIF-4A3	AT3G19760

VIT_06s0080g00560	Beta-alanine synthase	AT2G27450
VIT_06s0080g00570	Unknown protein	AT5G22390
VIT_06s0080g00580	Rac GTPase activating protein 1	AT5G22400
VIT_06s0080g00590	Harpin-induced protein	AT3G44380
VIT_06s0080g00600	No hit	-
VIT_06s0080g00610	No hit	-
VIT_06s0080g00630	No hit	-
VIT_06s0080g00640	No hit	-
VIT_07s0005g03470	Structural maintenance of chromosomes (SMC1)	AT3G54670
VIT_07s0005g03490	VHS domain-containing protein	AT1G06210
VIT_07s0005g03500	Serine-type peptidase	AT1G06200
VIT_07s0005g03510	SAP protein BP-73 E1-E2_ATPase	AT1G06190
VIT_07s0005g03520	Armadillo/beta-catenin repeat family protein	AT3G54790
VIT_07s0005g03530	Ribulose bisphosphate carboxylase, large chain	AT2G31160
VIT_07s0005g03540	Plastid-specific 50S ribosomal protein 6	AT5G17870
VIT_07s0005g03570	Arabinose-5-phosphate isomerase	AT3G54690
VIT_07s0005g03580	Transcription factor jumonji (jmj) / zinc finger (C5HC2 type)	AT1G08620
VIT_07s0005g03590	NADH dehydrogenase subunit 7	-
VIT_07s0005g03600	Transcription factor jumonji (jmj) / zinc finger (C5HC2 type)	AT1G08620
VIT_07s0005g03610	NAC domain-containing protein 74	AT4G28530
VIT_07s0005g03620	Serine/threonine kinase 19 isoform 1 STK19	AT2G20495
VIT_07s0005g03630	Ankyrin	AT1G04430
VIT_07s0005g03640	Asparagine N-glycosyltransferase	AT4G21150
VIT_07s0005g03660	Non-intrinsic ABC protein 4	AT1G03900
VIT_07s0005g03670	CHR8 (chromatin remodeling 8)	AT2G18760
VIT_07s0005g03680	CCR4-NOT complex subunit CAF16	AT1G03905
VIT_07s0005g03690	Protein kinase MK6	AT4G14350
VIT_07s0005g03700	Scarecrow transcription factor 23 (SCL23)	AT3G54220
VIT_07s0005g03710	Casein Kinase I-like 10	AT3G23340
VIT_07s0005g03720	VPS2.3 SNF7	AT1G03950
VIT_07s0005g03730	Protein phosphatase 2 (formerly 2A), regulatory subunit B"	AT5G44090
VIT_07s0005g03740	RabGAP/TBC domain-containing protein	AT2G20440
VIT_07s0005g03750	RIC7 (ROP-interactive crib motif-containing protein 7)	AT4G28560
VIT_07s0005g03760	Phytochelatin synthase 1 (PCS1)	AT5G44070
VIT_07s0005g03770	Expansin-A7	-
VIT_07s0005g03780	Alcohol oxidase	AT4G28570
VIT_07s0005g03790	Succinyl-CoA ligase beta-chain	AT2G20420
VIT_07s0005g03800	Unknown protein	AT4G28590
VIT_07s0005g03810	Unknown protein	AT5G44060
VIT_07s0005g03820	Acyl-[acyl-carrier-protein] desaturase	-

VIT_07s0005g03830	Calmodulin-binding protein	AT4G28600
VIT_07s0005g03840	Transcription termination factor mitochondrial mTERF	AT5G07900
VIT_07s0005g03850	No hit	-
VIT_07s0005g03860	Transcription termination factor mitochondrial mTERF	AT5G07900
VIT_07s0005g03870	Transcription termination factor mitochondrial mTERF	-
VIT_07s0005g03880	Transcription termination factor mitochondrial mTERF	-
VIT_07s0005g03890	Transcription termination factor mitochondrial mTERF	-
VIT_07s0005g03900	Rho GDP-dissociation inhibitor 1	AT3G07880
VIT_07s0005g03910	Phosphatidylcholine-sterol O-acyltransferase	AT1G04010
VIT_07s0005g03930	Developmental protein DAG, plastid	AT2G33430
VIT_07s0005g03940	ATBARD1/BARD1 (breast cancer associated ring 1)	
VIT_07s0005g03950	Ankyrin	AT3G54070
VIT_07s0005g03960	Peptide transporter protein 3	AT5G46050
VIT_07s0005g03970	Peptide transporter protein 3	AT5G46050
VIT_07s0005g03980	RNA-binding protein Musashi	AT4G14300
VIT_07s0005g03990	Unknown protein	AT1G04030
VIT_07s0005g04000	No hit	-
VIT_07s0005g04020	Leucine Rich Repeat receptor-like kinase	AT4G08850
VIT_07s0005g04040	Leucine Rich Repeat receptor-like kinase	AT4G08850
VIT_07s0005g04050	Leucine Rich Repeat receptor-like kinase	AT4G08850
VIT_07s0005g04060	Leucine Rich Repeat receptor-like kinase	AT4G08850
VIT_07s0005g04070	Leucine Rich Repeat receptor-like kinase	AT4G08850
VIT_07s0005g04080	Leucine Rich Repeat receptor-like kinase	AT4G08850
VIT_07s0005g04100	Leucine Rich Repeat receptor-like kinase	AT4G08850
VIT_07s0005g04110	Cellulose synthase CESA4	AT5G44030
VIT_07s0005g04120	PHR1 (phosphate starvation response 1)	AT4G28610
VIT_07s0005g04130	Acid phosphatase class B	AT5G44020
VIT_07s0005g04150	Ribosomal protein L23 (RPL23C) 60S	AT3G04400
VIT_07s0005g04180	Glutathione S-transferase	AT5G44000
VIT_07s0005g04190	Histone-lysine N-methyltransferase SUVR4	AT3G04380
VIT_07s0005g04200	No hit	-
VIT_07s0005g04210	No hit	-
VIT_07s0005g04220	Receptor-like protein kinase	AT1G04520
VIT_07s0005g04230	No hit	-
VIT_07s0005g04240	Import receptor subunit TOM22 homolog 2, Mitochondrial	AT5G43970
VIT_07s0005g06180	RPM1 (resistance to p. syringae pv maculicola 1)	AT3G07040
VIT_07s0005g06190	NADH dehydrogenase (ubiquinone) flavoprotein 2	AT4G02580
VIT_07s0005g06200	RPM1 (resistance to p. syringae pv maculicola 1)	AT3G07040
VIT_07s0005g06210	RPM1 (resistance to p. syringae pv maculicola 1)	AT3G07040
VIT_07s0005g06220	RPM1 (resistance to p. syringae pv maculicola 1)	AT3G07040

VIT_07s0005g06240	R protein MLA10	AT3G07040
VIT_07s0005g06250	R protein MLA10	AT3G07040
VIT_07s0005g06260	No hit	-
VIT_07s0005g06280	No hit	-
VIT_07s0005g06290	Cytochrome b5 isoform Cb5-C	AT2G32720
VIT_07s0005g06300	Phototropic-responsive NPH3	AT5G48800
VIT_07s0005g06310	BSD domain-containing protein	AT3G24820
VIT_07s0005g06340	Cyclin dependent kinase inhibitor KIP-related protein 3	AT5G48820
VIT_07s0005g06350	Photosystem II 47 kDa protein	ATCG00680
VIT_07s0005g06360	E3 ubiquitin-protein ligase PRT1	AT3G24800
VIT_07s0005g06370	No hit	-
VIT_07s0005g06380	LUG (LEUNIG)	AT2G32700
VIT_07s0005g06390	No hit	-
VIT_07s0005g06400	No hit	-
VIT_07s0005g06410	High-affinity K+ transporter 1 (HKT1)	-
VIT_07s0005g06420	Thioredoxin family	AT3G07090
VIT_07s0005g06430	Unknown	-
VIT_07s0005g06440	Drug/metabolite transporter DMT family transporter	AT3G07080
VIT_12s0028g00550	No hit	-
VIT_12s0028g00560	Unknown	-
VIT_12s0028g00570	Vacuolar protein sorting 16 VCL1 (vacuoleless 1)	AT2G38020
VIT_12s0028g00590	3-hydroxyisobutyryl-CoA hydrolase	AT1G06550
VIT_12s0028g00610	Aspartyl protease	AT3G59080
VIT_12s0028g00630	Hydroxyacylglutathione hydrolase 3	AT1G53580
VIT_12s0028g00640	NOL1/NOP2/sun	AT1G06560
VIT_12s0028g00670	Zinc knuckle	-
VIT_12s0028g00680	No hit	-
VIT_12s0028g00690	Auxin responsive SAUR protein	-
VIT_12s0028g00710	4-hydroxyphenylpyruvate dioxygenase	AT1G06570
VIT_12s0028g00720	Unknown protein	AT1G06590
VIT_12s0028g00740	Unknown protein	AT1G06590
VIT_12s0028g00810	Unknown protein	AT1G06590
VIT_12s0028g00830	Pleckstriny (PH) domain-containing protein	AT2G30880
VIT_12s0028g00860	NAC domain-containing protein 42	AT2G43000
VIT_12s0028g00900	No hit	-
VIT_12s0028g00910	No hit	-
VIT_12s0028g00920	Glutathione S-transferase 9 GSTF9	AT2G30860
VIT_12s0028g00930	Glutathione S-transferase 9 GSTF9	AT2G30860
VIT_12s0028g00940	Electron transfer flavoprotein alpha-subunit precursor (Alpha-ETF)	AT1G06660
VIT_12s0028g00960	Phytoene synthase, chloroplast precursor	AT5G17230

VIT_12s0028g00980	Myb family	AT2G40260
VIT_12s0028g01000	Unknown protein	AT4G19645
VIT_12s0028g01010	Unknown	-
VIT_12s0028g01020	No hit	-
VIT_12s0028g01030	Unknown	-
VIT_12s0028g01040	Protein kinase	AT3G57750
VIT_12s0028g01050	Helicase in vascular tissue and TAPETUM	AT2G30800
VIT_12s0028g01060	No hit	-
VIT_12s0028g01070	WD-repeat protein 26	AT5G08560
VIT_12s0028g01080	Photosystem II oxygen-evolving complex precursor, 23kda PSBP	AT1G06680
VIT_12s0028g01090	Reticulon family protein (RTNLB5)	AT3G10260
VIT_12s0028g01100	Aldo/keto reductase	AT1G06690
VIT_12s0028g01110	Phytochrome- interacting factor 5 PIL6	AT2G43010
VIT_12s0028g01120	Amine oxidase	AT2G43020
VIT_12s0028g01130	No hit	-
VIT_12s0028g01140	Pentatricopeptide (PPR) repeat-containing protein	AT3G59040
VIT_12s0055g00750	Pentatricopeptide (PPR) repeat-containing protein	AT3G62470
VIT_12s0055g00760	No hit	-
VIT_12s0055g00770	SWAP (Suppressor-of-White-APricot)	AT4G31200
VIT_12s0055g00780	VPS20.2 SNF7	AT5G09260
VIT_12s0055g00790	Clathrin assembly protein 3	AT4G02650
VIT_12s0055g00800	Arachidonic acid-induced DEA1	AT1G12090
VIT_12s0055g00810	Cationic peroxidase	AT4G25980
VIT_12s0055g00820	Serine carboxypeptidase II	AT5G42240
VIT_12s0055g00830	Methyltransferase	AT3G26410
VIT_12s0055g00840	Sucrose-6-phosphate phosphatase	AT2G35840
VIT_12s0055g00850	Nodulin	AT3G43660
VIT_12s0055g00860	Nodulin	AT1G76800
VIT_12s0055g00870	Nodulin	AT1G76800
VIT_12s0055g00890	No hit	-
VIT_12s0055g00900	RAE1 RNA export 1 homolog	AT1G80670
VIT_12s0055g00910	Kelch repeat-containing F-box protein	AT1G22040
VIT_12s0055g00920	Aspartate aminotransferase	AT2G13810
VIT_12s0055g00930	Heavy-metal-associated domain-containing protein	AT2G28660
VIT_12s0055g00940	Sulfate transporter 1.2	AT1G78000
VIT_12s0055g00950	Receptor-like kinase 902	AT2G26730
VIT_12s0055g00960	Unknown	-
VIT_12s0055g00970	Pentatricopeptide repeat	AT2G15630
VIT_12s0055g00980	Peroxidase precursor	AT5G39580
VIT_12s0055g00990	Peroxidase	AT5G64120

VIT_12s0055g01000	Peroxidase	AT5G39580
VIT_12s0055g01010	Peroxidase	AT5G64120
VIT_12s0055g01020	Peroxidase	AT5G39580
VIT_12s0055g01030	Peroxidase	AT5G64120
VIT_14s0066g00920	Polyribonucleotide nucleotidyltransferase	AT5G14580
VIT_14s0066g00950	Isocitrate dehydrogenase, chloroplast precursor	AT5G14590
VIT_14s0066g00960	Glutaredoxin	AT5G40370
VIT_14s0066g00970	Anthranilate phosphoribosyltransferase, chloroplast precursor	AT5G17990
VIT_14s0066g00980	Unknown protein	AT5G62960
VIT_14s0066g00990	TRNA methyltransferase complex GCD14 subunit	AT5G14600
VIT_14s0066g01000	Phosphate/phosphoenolpyruvate translocator	AT3G01550
VIT_14s0066g01010	Myb domain protein 98	AT4G18770
VIT_14s0066g01020	DEAD box RNA helicase 1	AT3G01540
VIT_14s0066g01030	Tubulin gamma complex component 2	AT5G17410
VIT_14s0066g01040	Cytosine methyltransferase (DRM2)	AT5G14620
VIT_14s0066g01050	Glycogen synthase kinase 3 beta	AT5G14640
VIT_14s0066g01060	Polygalacturonase GH28	AT5G14650
VIT_14s0066g01070	Peptide deformylase, chloroplast precursor	AT5G14660
VIT_14s0066g01080	ADP-ribosylation factor A1B	AT5G14670
VIT_14s0066g01090	Myb domain protein 24	AT5G40350
VIT_14s0066g01100	Monodehydroascorbate reductase, cytoplasmic isoform 2	AT3G27820
VIT_14s0066g01110	Ribosomal protein L12-1, chloroplast (CL12-A) 50S	AT3G27830
VIT_14s0066g01120	PWWP domain-containing protein	AT5G40340
VIT_14s0066g01130	Universal stress protein A	AT5G14680
VIT_14s0066g01140	Unknown protein	-
VIT_14s0066g01150	Cinnamoyl-CoA reductase	AT5G14700
VIT_14s0066g01160	Unknown protein	AT5G14710
VIT_14s0066g01170	MAP4K alpha1	AT5G14720
VIT_14s0066g01180	Phospholipid-transporting ATPase	AT3G27870
VIT_14s0066g01190	Unknown protein	AT3G27880
VIT_14s0066g01200	Protein kinase beta-1 subunit 5'-AMP-activated	AT3G01510
VIT_14s0066g01210	Carbonic anhydrase, chloroplast precursor	AT3G01500
VIT_14s0066g01220	ATMYB66/WER/WER1 (WEREWOLF 1)	AT5G14750
VIT_14s0066g01230	Unknown protein	AT3G27930
VIT_14s0066g01240	L-aspartate oxidase	AT5G14760
VIT_14s0066g01250	Alpha-L-fucosidase 2 precursor	-
VIT_14s0066g01260	Lipase GDSL	AT3G27950
VIT_14s0066g01270	Alpha-L-fucosidase 2 precursor	AT5G14450
VIT_14s0066g01280	Kinesin light chain	AT3G27960
VIT_14s0066g01290	Exonuclease	AT3G27970

VIT_14s0066g01300	Unknown protein	AT2G36330
VIT_14s0066g01310	CAAX farnesyltransferase beta subunit	AT5G40280
VIT_14s0066g01320	formate dehydrogenase (FDH)	AT5G14780
VIT_14s0066g01330	No hit	-
VIT_14s0066g01340	DNA-binding protein	AT1G23750
VIT_14s0066g01350	No hit	-
VIT_14s0066g01360	No hit	-
VIT_14s0066g01370	No hit	-
VIT_14s0066g01380	Calcium homeostasis regulator CHoR1	AT3G55250
VIT_14s0066g01390	Metal-dependent phosphohydrolase HD domain-containing protein	AT5G40270
VIT_14s0066g01400	MLK/Raf-related protein kinase 1	AT3G01490
VIT_14s0066g01410	Peptidylprolyl isomerase	AT3G01480
VIT_14s0066g01420	Nodulin MtN3 family	AT3G28007
VIT_14s0066g01430	Unknown protein	AT2G23470
VIT_14s0066g01440	Homeodomain leucine zipper protein HB-1	AT3G01470
VIT_14s0066g01450	MBD9 (methyl-CPG-binding Domain 9)	AT3G01460
VIT_14s0066g01460	HEAT repeat-containing protein	AT5G14790
VIT_14s0066g01470	Binding	-
VIT_14s0066g01480	Cis-zeatin O-beta-D-glucosyltransferase	AT5G14860
VIT_14s0066g01490	UDP-glucoronosyl and UDP-glucosyl transferase	AT2G16890
VIT_14s0066g01500	UDP-glucoronosyl and UDP-glucosyl transferase	AT2G16890
VIT_14s0066g01520	UDP-glucoronosyl and UDP-glucosyl transferase	AT5G14860
VIT_14s0066g01530	No hit	-
VIT_14s0066g01540	Serine/threonine kinase SYMRK	AT1G49100
VIT_14s0066g01550	Aldehyde dehydrogenase 1 precursor	AT1G23800
VIT_14s0066g01560	Cyclic nucleotide-gated ion channel 18	AT5G14870
VIT_14s0066g01570	Unknown protein	AT1G23840
VIT_14s0066g01580	K+ uptake permease 6	AT5G14880
VIT_14s0066g01590	NHL repeat-containing protein	AT1G70280
VIT_14s0066g01600	NHL repeat-containing protein	AT5G14890
VIT_14s0066g01610	Zinc finger (C3HC4-type ring finger)	AT5G40250
VIT_14s0066g01620	Hypoxia-responsive	AT3G48030
VIT_14s0066g01630	UVH3 (ultraviolet hypersensitive 3)	AT3G28030
VIT_14s0066g01640	Nodulin MtN21 family	AT5G40230
VIT_14s0066g01650	Nodulin MtN21 family	AT3G28050
VIT_14s0066g01660	DegP protease	AT5G40200
VIT_14s0066g01670	Alpha-dioxygenase	AT3G01420
VIT_14s0066g01680	No hit	-
VIT_14s0066g01690	Pathogen-inducible alpha-dioxygenase	AT3G01420
VIT_14s0066g01700	Calmodulin binding protein	AT5G40190

VIT_14s0066g01710	Leaf senescence protein	AT3G28150
VIT_14s0066g01720	Bromo-adjacenty (BAH) domain-containing protein	AT3G48050
VIT_14s0066g01730	Cellulose synthase CSLC04	AT3G28180
VIT_14s0066g01740	Unknown protein	AT1G22270
VIT_14s0066g01750	EMB506 ankyrin repeat protein	AT5G40160
VIT_14s0066g01780	Heavy-metal-associated domain-containing protein	AT5G14910
VIT_14s0066g01790	GASA like	AT5G14920
VIT_14s0066g01800	Phosphatidylinositolglycan class N (PIG-N)	AT3G01380
VIT_14s0066g01810	SAG101 (senescence-associated gene 101)	AT5G14930
VIT_14s0066g01820	SAG101 (senescence-associated gene 101)	AT5G14930
VIT_14s0066g01830	SAG101 (senescence-associated gene 101)	AT5G14930
VIT_14s0066g01840	SAG101 (senescence-associated gene 101)	AT5G14930
VIT_18s0001g14060	Transposon protein, CACTA, En/Spm sub-class	AT3G11290
VIT_18s0001g14070	Unknown	-
VIT_18s0001g14080	Diphthine synthase (DPH5)	AT4G31790
VIT_18s0001g14090	Molecular chaperone DnaJ	AT1G75690
VIT_18s0001g14100	ABA-responsive protein (HVA22) HVA22H	AT5G42560
VIT_18s0001g14110	Transcription factor E2F/dimerisation partner (TDP) E2F2	AT1G47870
VIT_18s0001g14120	Translation initiation factor eIF-3 subunit 3	AT2G45730
VIT_18s0001g14130	Zinc finger (C2H2 type) family	AT1G75710
VIT_18s0001g14140	No hit	-
VIT_18s0001g14150	No hit	-
VIT_18s0001g14160	Heat-and acid-stable phosphoprotein	-
VIT_18s0001g14170	Cyclin-dependent protein kinase regulator CYCB2_4	AT1G76310
VIT_18s0001g14180	Armadillo/beta-catenin repeat family protein	AT5G42340
VIT_18s0001g14190	Unknown	-
VIT_18s0001g14200	No hit	-
VIT_18s0001g14210	Unknown protein	AT1G75720
VIT_18s0001g14230	Hexokinase	AT1G47840
VIT_18s0001g14240	Adaptor-related protein complex 2, sigma 1 sub	AT1G47830
VIT_18s0001g14250	Unknown protein	-
VIT_18s0001g14260	No hit	-
VIT_18s0001g14270	Gibberellin-regulated protein 1 (GASA1)	AT1G75750
VIT_18s0001g14280	ER lumen protein retaining receptor	AT1G75760
VIT_18s0001g14290	Invertase-like protein	AT4G34860
VIT_18s0001g14300	Cytomatrix protein	AT1G19980
VIT_18s0001g14310	Flavonone- 3-hydroxylase	AT3G51240
VIT_18s0001g14320	Unknown protein	AT1G19990
VIT_18s0001g14330	No hit	-
VIT_18s0001g14340	No hit	-

VIT_18s0001g14350	No hit	-
VIT_18s0001g14360	Tubulin beta-1 chain	AT1G75780
VIT_18s0001g14370	No hit	-
VIT_18s0001g14380	Brain and reproductive organ-expressed protein	AT5G42470
VIT_18s0001g14390	Transducin protein	AT3G06880
VIT_18s0001g14400	Peptidyl-prolyl cis-trans isomerase ROC5 (rotamase CYP 5)	AT4G34870
VIT_18s0001g14410	Unknown protein	AT1G30755
VIT_18s0001g14420	Unknown	-
VIT_18s0001g14430	Unknown	-
VIT_18s0001g14440	Molecular chaperone DnaJ	AT4G36040
VIT_18s0001g14450	Ferredoxin: nadp+ Oxidoreductase PETH	AT5G66190
VIT_18s0001g14460	Unknown protein	AT4G24175
VIT_18s0001g14470	No hit	-
VIT_18s0001g14480	Thaumatin SCUTL1	AT1G20030
VIT_18s0001g14490	Thaumatin	AT4G24180
VIT_18s0001g14500	SHD (shepherd)	AT4G24190
VIT_18s0001g14510	Ribosomal protein L28	AT4G31460
VIT_18s0001g14520	Unknown protein	AT1G75810
VIT_18s0001g14530	Ubiquitin-protein ligase CIP8 (COP1-interacting protein 8)	AT5G64920
VIT_18s0001g14540	DEAD-box ATP-dependent RNA helicase 28	AT4G16630
VIT_18s0001g14550	Unknown protein	AT4G24200
VIT_18s0001g14560	Unknown	-
VIT_18s0001g14580	Kinesin family member 18/19	AT1G20060
VIT_18s0001g14590	ATSYTC/NTMC2T1.3/NTMC2TYPE1.3/SYTC	AT5G04220
VIT_18s0001g14600	Pentatricopeptide (PPR) repeat-containing protein	-
VIT_18s0001g14610	Clavata1 receptor kinase (CLV1)	AT1G75820
VIT_18s0001g14620	Ribosomal protein S16	-
VIT_18s0001g14630	ATSYTB/NTMC2T1.2/NTMC2TYPE1.2/SYTB	AT1G20080
VIT_18s0001g14640	No hit	-
VIT_18s0001g14650	DNA-directed RNA polymerase I subunit A12	-
VIT_18s0001g14660	P-glycoprotein 13	AT1G27940
VIT_18s0001g14670	Rac-like GTP-binding protein RAC1	AT1G75840
VIT_18s0001g14680	Vacuolar protein sorting 35	AT1G75850
VIT_18s0001g14690	Protein kinase	AT1G77280
VIT_18s0001g14700	Unknown	-
VIT_18s0001g14710	Ketol-acid reductoisomerase precursor	AT3G58610
VIT_18s0001g14720	Ankyrin repeat family protein	-
VIT_18s0001g14730	Glutaredoxin	AT5G42150
VIT_18s0001g14740	Protein binding	-
VIT_18s0001g14750	Zinc finger (FYVE type) VPS19	AT1G20110

VIT_18s0001g14760	Lipase 3 (EXL3) family II extracellular	AT1G75900
VIT_18s0001g14770	Lipase 3 (EXL3) family II extracellular	AT1G75900
VIT_18s0001g14780	Lipase 3 (EXL3) family II extracellular	AT1G75900
VIT_18s0001g14790	Lipase 3 (EXL3) family II extracellular	AT1G75900
VIT_18s0001g14800	Lipase 3 (EXL3) family II extracellular	AT1G75900
VIT_18s0001g14810	Lipase 3 (EXL3) family II extracellular	AT1G75900
VIT_18s0001g14840	Nickel ion transporter	AT2G16800
VIT_18s0001g14850	Unknown protein	AT1G11320
VIT_18s0001g14860	SKP1	AT5G42190
VIT_18s0001g14870	Subtilisin-type protease precursor	AT1G20160
VIT_18s0001g14880	Unknown protein	AT4G22000
VIT_18s0001g14890	ABA-responsive element-binding protein 3 (AREB3)	-
VIT_18s0001g14900	La domain-containing protein	AT4G35890
VIT_18s0001g14910	Mannitol dehydrogenase	AT4G39330
VIT_18s0001g14920	Unknown protein	AT1G20180
VIT_18s0001g14930	Unknown protein	AT1G75980
VIT_18s0001g14940	Pentatricopeptide (PPR) repeat-containing	AT3G26540
VIT_18s0001g14950	EMB2170 (embryo defective 2170)	AT1G76980
VIT_18s0001g14960	Pentatricopeptide (PPR) repeat-containing	AT1G77010
VIT_18s0001g14970	Pentatricopeptide (PPR) repeat-containing	AT1G43980
VIT_18s0001g14980	3-methyl-2-oxobutanoate dehydrogenase	AT1G21400
VIT_18s0001g14990	Dual-specific kinase DSK1	AT3G13690
VIT_18s0001g15000	ACT domain containing protein (ACR4)	AT1G76990
VIT_18s0001g15010	F-box and leucine-rich repeat protein 1	AT1G77000
VIT_18s0001g15020	DnaJ homolog, subfamily A, member 4	AT1G77020
VIT_18s0001g15050	Protein phosphatase 2C	AT1G43900
VIT_18s0001g15060	No hit	-
VIT_18s0001g15070	No hit	-
VIT_18s0001g15080	No hit	-
VIT_18s0001g15090	RAB GTPase RAB18	AT1G43890
VIT_18s0001g15100	flavin-containing monooxygenase, putative	AT1G48910
VIT_18s0001g15110	Flavin-containing monooxygenases	AT1G21430
VIT_18s0001g15120	Unknown protein	AT4G19950
VIT_18s0001g15130	WD40 repeat protein	-
VIT_18s0001g15140	Unknown	-
VIT_18s0001g15150	Unknown protein	-
VIT_18s0001g15160	S-adenosylmethionine sythetase 2	AT4G01850
VIT_18s0001g15170	S-adenosylmethionine sythetase 2	AT4G01850
VIT_18s0001g15180	No hit	-
VIT_18s0001g15190	flavin-containing monooxygenase, putative	AT1G48910

VIT_18s0001g15200	SIK1 (serine/threonine kinase 1)	-
VIT_18s0001g15220	Unknown protein	AT1G31130
VIT_18s0001g15230	Unknown	-
VIT_18s0001g15240	Blue (type 1) copper domain	AT2G02850
VIT_18s0001g15250	Unknown	-
VIT_18s0001g15260	Myb domain protein 52	AT1G17950
VIT_18s0001g15270	SCL1 (scarecrow-like 1)	AT1G21450
VIT_18s0001g15280	RNA exonuclease 1	AT5G25800
VIT_18s0001g15290	Ribosome maturation protein SDO1	AT1G43860
VIT_18s0001g15300	No hit	-
VIT_18s0001g15310	Thioredoxin M-type	AT3G15360
VIT_18s0001g15320	SEU3B protein	AT1G43850
VIT_18s0001g15330	SWEET1	AT1G21460
VIT_18s0001g15340	Pentatricopeptide (PPR) repeat-containing protein	-
VIT_18s0001g15350	Pentatricopeptide (PPR) repeat-containing protein	AT3G21470
VIT_18s0001g15360	Thylakoid lumenal 29.8 kDa protein	AT1G77090
VIT_18s0001g15370	Exostosin family protein	AT1G21480
VIT_18s0001g15380	No hit	-
VIT_18s0001g15390	Gaiacol peroxidase	AT4G25980
VIT_18s0001g15400	KOW domain-containing transcription factor family protein	AT4G08350
VIT_18s0001g15410	Alcohol dehydrogenase 1	AT1G77120
VIT_18s0001g15420	Auxin efflux carrier protein 6	AT1G77110
VIT_18s0001g15430	Alliin lyase	-
VIT_18s0001g15450	Alcohol dehydrogenase 3	AT1G77120
VIT_18s0001g15460	Stearyl acyl carrier protein desaturase	AT1G43800
VIT_18s0001g15470	Leaf senescence related protein-like	AT1G48880
VIT_18s0001g15510	Unknown	-
VIT_18s0001g15520	Leaf senescence protein	AT1G48880
VIT_18s0001g15530	Pentatricopeptide (PPR) repeat-containing	AT3G09040
VIT_18s0001g15540	No hit	-
VIT_18s0001g15550	Serine carboxypeptidase II	AT5G42240
VIT_18s0001g15560	Unknown protein	AT1G77122
VIT_18s0001g15570	Zinc finger (CCCH-type) family protein	AT3G18640
VIT_18s0001g15580	Glycogenin glucosyltransferase (glycogenin)	AT1G77130
VIT_18s0001g15600	Vacuolar protein sorting 45	AT1G77140
VIT_18s0001g15610	Unknown	-
VIT_18s0001g15620	Receptor kinase TRKe	AT3G47090
VIT_18s0001g15630	MAP kinase activating protein	AT1G77220
VIT_18s0001g15640	Pathogenesis-related	AT1G78780
VIT_18s0001g15650	Pathogenesis related protein	AT1G78780

VIT_18s0001g15660	Pathogen-related	AT1G78780
VIT_18s0001g15670	Cytoplasm protein	AT1G21370
VIT_18s0001g15680	Cellulase	AT4G24260
VIT_18s0001g15690	Endo-1,4-beta-glucanase	-
VIT_18s0001g15700	GLTP3 (glycolipid transfer protein 3)	AT3G21260
VIT_18s0001g15710	Electron carrier/ oxidoreductase	AT1G21350
VIT_18s0001g15720	Leucine Rich Repeat receptor-like kinase	AT3G24240
VIT_18s0001g15730	Dof zinc finger protein DOF3.5	AT3G52440
VIT_18s0001g15740	No hit	-
VIT_18s0001g15750	Protein kinase Xa21	AT3G47110
VIT_18s0001g15760	Copine BON3 (BONZAI 3)	-
VIT_18s0001g15790	V-type H+-transporting ATPase 16kDa proteolipid subunit	-
VIT_18s0001g15800	Protein kinase Xa21	AT3G47570
VIT_18s0166g00020	RWP-RK domain-containing protein	-
VIT_18s0166g00030	No hit	-
VIT_18s0166g00040	Protein kinase Xa21	AT3G47570
VIT_18s0166g00050	EFR (EF-TU receptor)	AT3G47570
VIT_18s0166g00060	No hit	
VIT_18s0166g00070	No hit	-

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Gene stable ID	**Functional annotation**	**Arabidopsis homolog**
VIT_02s0012g02590	Galacturonosyltransferase 1	-
VIT_02s0012g02600	Octicosapeptide/Phox/Bem1p (PB1) domain-containing protein	-
VIT_02s0012g02610	SAR1 (suppressor of auxin resistance1) (Nup160)	-
VIT_02s0012g02620	PFT1 (phytochrome and flowering time 1) MED25	-
VIT_02s0012g02640	Aspartic-type endopeptidase	-
VIT_02s0012g02650	Purple acid phosphatase 2 PAP2	-
VIT_02s0012g02660	Proteasome 26S regulatory subunit (RPN9)	AT5G45620
VIT_02s0012g02670	Unknown protein	AT1G31940
VIT_02s0012g02720	RPM1 (resistance to p. syringae pv maculicola 1)	AT3G07040
VIT_02s0012g02760	Methionyl-tRNA synthetase	AT4G13780
VIT_02s0012g02770	ABC transporter g family pleiotropic drug resistance 12 PDR12	AT1G15520
VIT_02s0012g02780	Cytochrome b5 domain-containing protein	AT4G14965
VIT_02s0012g02790	Secretory carrier membrane protein (SCAMP4)	AT1G32050
VIT_02s0012g02800	No hit	-
VIT_02s0012g02810	CYP76C4	AT2G45550
VIT_02s0012g02820	Geraniol 10-hydroxylase	AT2G45550
VIT_02s0012g02830	UDP-glucosyl transferase	AT3G02100
VIT_02s0012g02840	No hit	-
VIT_02s0154g00080	Multi-copper oxidase (SKU5)	AT4G12420
VIT_02s0154g00090	Vacuolar invertase 2, GIN2	AT1G12240
VIT_02s0154g00100	Transaldolase totaL2	AT1G12230
VIT_02s0154g00110	Trehalose-6-phosphate phosphatase (AtTPPA)	AT4G12430
VIT_02s0154g00120	Unknown	AT4G22600
VIT_02s0154g00130	Exostosin (Xyloglucan galactosyltransferase KATAMARI 1)	AT4G22580
VIT_02s0154g00140	3-oxoacyl-[acyl-carrier-protein] synthase 3 A, chloroplast precursor	AT1G62640
VIT_02s0154g00150	PLATZ transcription factor	AT3G60670
VIT_02s0154g00160	flavin-containing monooxygenase family protein / FMO family protein	AT1G62600
VIT_02s0154g00170	flavin-containing monooxygenase 3	-
VIT_02s0154g00180	flavin-containing monooxygenase 3	AT1G62600
VIT_02s0154g00190	flavin-containing monooxygenase 3	AT1G62620
VIT_02s0154g00200	Unknown protein	AT1G12120
VIT_02s0154g00210	WRKY DNA-binding protein 21	AT2G30590
VIT_02s0154g00220	Zinc finger (C2H2 type) family	AT1G62520
VIT_02s0154g00230	Phosphatidic acid phosphatase / PAP2	AT4G22550
VIT_02s0154g00300	Small nuclear ribonucleoprotein Sm D3	AT1G12090
VIT_02s0154g00310	Protease inhibitor/seed storage/lipid transfer protein (LTP)	AT1G62500
VIT_02s0154g00320	Protease inhibitor/seed storage/lipid transfer protein (LTP)	AT2G45180

VIT_02s0154g00330	Unknown protein	AT5G47570
VIT_02s0154g00340	No hit	-
VIT_02s0154g00350	L-lactate dehydrogenase A	AT4G17260
VIT_02s0154g00360	No hit	-
VIT_02s0154g00370	YbaK/prolyl-tRNA synthetase associated region	AT4G16510
VIT_02s0154g00380	Unknown	-
VIT_02s0154g00390	Autophagy 8f (APG8f)	AT4G16520
VIT_02s0154g00400	Scarecrow transcription factor 6 (SCL6)	AT4G00150
VIT_02s0154g00410	Unknown protein	AT5G47580
VIT_02s0154g00420	No hit	-
VIT_02s0154g00430	Unknown	-
VIT_02s0154g00440	Unknown protein	AT5G47580
VIT_02s0154g00450	Zinc knuckle	-
VIT_02s0154g00460	Unknown protein	AT4G16530
VIT_02s0154g00470	No hit	-
VIT_02s0154g00480	Heat shock protein MTSHP	AT4G25200
VIT_02s0154g00490	Heat shock 22 kDa protein mitochondrial	AT4G25200
VIT_02s0154g00500	VAP27-1 (VAMP/synaptobrevin-associated protein 27-1)	AT3G60600
VIT_02s0154g00510	SEC14 cytosolic factor	AT5G47510
VIT_02s0154g00520	Aspartyl protease	AT4G16563
VIT_02s0154g00530	Histidine triad nucleotide binding protein 3	AT4G16566
VIT_02s0154g00540	Protein arginine N-methyltransferase	AT4G16570
VIT_02s0154g00550	DnaJ homolog, subfamily C, member 11	AT2G35720
VIT_02s0236g00160	Serine/threonine Phosphatase 7	-
VIT_02s0236g00170	No hit	-
VIT_02s0241g00070	Zinc finger (DHHC type)	AT3G60800
VIT_02s0241g00080	Glycine-rich protein-like	AT4G22740
VIT_02s0241g00090	Translation release factor	AT1G62850
VIT_02s0241g00100	Unknown protein	AT2G45360
VIT_02s0241g00110	Aminomethyltransferase	AT4G12130
VIT_02s0241g00120	Receptor protein kinase	AT4G22730
VIT_02s0241g00130	No hit	-
VIT_02s0241g00140	Calmodulin (A)	AT1G12310
VIT_02s0241g00150	No hit	-
VIT_02s0241g00160	Esterase/lipase/thioesterase family	AT4G12230
VIT_02s0241g00170	Zinc finger (C2H2 type) family	AT4G12240
VIT_02s0241g00180	UDP-D- glcucuronate 4-epimerase 5 GAE5	AT4G12250
VIT_02s0241g00190	No hit	-
VIT_02s0488g00010	H (+)-ATPase 4 AHA4	AT5G62670
VIT_02s0488g00020	Palmitoyl-protein thioesterase 1 precursor	AT3G60340

VIT_02s0488g00030	No hit	-
VIT_02s0488g00040	Pentatricopeptide repeat-containing protein	-
VIT_02s0488g00050	Dual specificity phosphatase	-
VIT_04s0008g00190	ATP-dependent protease La (LON) domain-containing	AT2G25740
VIT_04s0008g00200	Tryptophan-tRNA ligase	AT2G25840
VIT_04s0008g00210	Histidine-containing phosphotransferase	AT3G16360
VIT_04s0008g00220	IAA6	AT3G16500
VIT_04s0008g00230	Amino acid permease 8	AT1G10010
VIT_04s0008g00240	Amino acid permease 6	AT5G49630
VIT_04s0008g00250	Amino acid permease 6	AT5G49630
VIT_04s0008g00260	Amino acid permease 6	AT5G49630
VIT_04s0008g00270	Elongation factor 1-alpha (EF-1-alpha)	AT5G60390
VIT_04s0008g00280	Amino acid permease 1	AT1G58360
VIT_04s0008g00290	Clavata1 receptor kinase (CLV1)	AT5G25930
VIT_04s0008g00300	Clavata1 receptor kinase (CLV1)	AT5G25930
VIT_04s0008g00310	Clavata1 receptor kinase (CLV1)	AT5G25930
VIT_04s0008g00320	Leucine-rich repeat family protein	-
VIT_04s0008g00330	Clavata1 receptor kinase (CLV1)	AT5G25930
VIT_04s0008g00340	Clavata1 receptor kinase (CLV1)	AT5G25930
VIT_04s0008g00350	Clavata1 receptor kinase (CLV1)	AT5G25930
VIT_04s0008g00370	Clavata1 receptor kinase (CLV1)	AT5G25930
VIT_04s0008g00380	No hit	-
VIT_04s0008g00390	Clavata1 receptor kinase (CLV1)	AT5G25930
VIT_04s0008g00400	Clavata1 receptor kinase (CLV1)	AT5G25930
VIT_04s0008g00410	Clavata1 receptor kinase (CLV1)	AT5G25930
VIT_04s0008g00420	Clavata1 receptor kinase (CLV1)	AT5G25930
VIT_04s0008g00430	Clavata1 receptor kinase (CLV1)	AT5G25930
VIT_04s0008g00440	Clavata1 receptor kinase (CLV1)	AT5G25930
VIT_04s0008g00450	Haloacid dehalogenase hydrolase	AT2G25870
VIT_04s0008g00740	Protein phosphatase 2C	AT5G26010
VIT_04s0008g00750	Unknown protein	AT4G32960
VIT_04s0008g00760	Thioredoxin Trp26	AT2G25950
VIT_04s0008g00770	Glycine hydroxymethyltransferase	AT4G32520
VIT_04s0008g00780	Unknown	-
VIT_04s0008g00790	Ribosomal protein L28 (RPL28C) 60S	AT2G19730
VIT_04s0008g00800	Ferrochelatase-2	AT5G26030
VIT_04s0008g00810	ATP synthase g subunit mitochondrial	AT4G29480
VIT_04s0008g00820	KH domain-containing protein	AT2G25970
VIT_04s0008g00830	NADH dehydrogenase (ubiquinone) Fe-S protein 7	AT5G11770
VIT_04s0008g00840	Ser/Thr specific protein phosphatase 2A B regulatory subunit beta isoform	AT1G17720

VIT_04s0008g00900	MYB divaricata	AT5G56840
VIT_04s0008g00910	Histone deacetylase protein (HDA2)	AT5G26040
VIT_04s0008g00920	Clavata1 receptor kinase (CLV1)	AT5G25930
VIT_04s0008g00930	Alpha-expansin 6 precursor	-
VIT_04s0008g00950	Calcineurin B protein 10	AT4G33000
VIT_04s0008g00960	Calcineurin B protein 10	AT4G33000
VIT_04s0008g00970	Translation initiation factor eIF-4A	-
VIT_04s0008g00980	Translation initiation factor eIF-4A	-
VIT_04s0008g00990	Translation initiation factor eIF-4A	AT3G13920
VIT_04s0008g01000	EIF-4A3	AT3G13920
VIT_04s0008g01010	No hit	-
VIT_04s0008g01020	Unknown protein	AT5G11970
VIT_04s0008g01030	Unknown protein	AT5G11960
VIT_04s0008g01040	Lysine decarboxylase	AT5G11950
VIT_04s0008g01050	Unknown	-
VIT_04s0008g01060	Substrate carrier, Mitochondrial	AT1G14560
VIT_04s0008g01070	Calmodulin-binding region IQD6	AT2G26190
VIT_04s0008g01080	Calmodulin-binding region IQD6	AT2G26180
VIT_04s0008g01090	CYP706A12	AT2G26170
VIT_04s0008g01100	CYP706A12	AT2G26170
VIT_04s0008g01110	Heat shock transcription factor A6B	AT2G26150
VIT_04s0008g01120	Glutaredoxin	AT4G33040
VIT_04s0008g01130	Solute carrier family 25	AT5G56450
VIT_04s0008g01350	Conserved oligomeric Golgi complex component 8	AT5G11980
VIT_04s0008g01360	Tassel serine threonine kinase 1	AT5G12000
VIT_04s0008g01370	Peptidyl-prolyl cis-trans isomerase SDCCAG10	AT4G33060
VIT_04s0008g01380	Unknown protein	AT5G12010
VIT_04s0008g01390	RNA recognition motif (RRM)-containing protein	AT1G21312
VIT_04s0008g01400	Protein kinase MK6	AT4G33080
VIT_04s0008g01410	Ran-binding protein 1 RanBP1	AT5G58590
VIT_04s0008g01420	HAB2 (Homology to ABI2)	AT1G17550
VIT_04s0008g01430	APM1 (Aminopeptidase M1)	AT4G33090
VIT_04s0008g01440	UPF0203 protein	AT4G33100
VIT_04s0008g01450	Cyclopropane-fatty-acyl-phospholipid synthase	AT4G33110
VIT_04s0008g01460	Unknown protein	AT5G26160
VIT_04s0008g01470	WRKY DNA-binding protein 50	AT5G26170
VIT_04s0008g01480	NOL1/NOP2/sun family protein	AT5G26180
VIT_04s0008g01630	No hit	-
VIT_04s0008g01640	Ankyrin repeat	-
VIT_04s0008g01650	Ankyrin repeat	AT5G51160

VIT_04s0008g01660	Carrier protein, Mitochondrial	AT1G72820
VIT_04s0008g01670	PHD finger protein alfin	AT5G26210
VIT_04s0008g01680	EMB2745	AT5G39710
VIT_04s0008g01690	Carbon-nitrogen hydrolase	AT5G12040
VIT_04s0008g01700	Unknown protein	AT1G54200
VIT_04s0008g01710	MAP3K delta-1 protein kinase	AT4G38470
VIT_04s0008g01720	Mechanosensitive ion channel	AT5G12080
VIT_04s0008g01730	PSBX (photosystem II subunit X)	-
VIT_04s0008g01740	Spermine synthase ACAULIS5	AT5G19530
VIT_04s0008g01750	Ribosomal protein S3 (RPS3C) 40S	AT5G35530
VIT_04s0008g01800	Myb domain protein 7	AT4G38620
VIT_04s0008g01810	Myb domain protein 4	AT4G38620
VIT_04s0008g01820	TT2 (transparent testa 2)	AT5G35550
VIT_04s0008g01830	Myb domain protein 32	AT4G34990
VIT_04s0008g01840	TT2 (transparent testa 2)	AT5G35550
VIT_04s0008g01850	Trihelix DNA-binding protein (GT2)	AT1G76880
VIT_04s0008g01860	CYP72A58	AT3G14690
VIT_04s0008g01870	ATMYB66/WER/WER1 (WEREWOLF 1)	AT5G14750
VIT_04s0008g01880	Cytokinin dehydrogenase 7	AT5G21482
VIT_04s0008g01890	F-box family protein (FBL15)	AT4G33210
VIT_04s0008g01900	Unknown protein	AT2G26340
VIT_04s0008g01910	ferredoxin-related	AT1G02180
VIT_04s0008g01920	F-box/LRR-repeat protein 20	AT2G06040
VIT_04s0008g01940	Unknown	-
VIT_04s0008g01950	YGGT	AT5G21920
VIT_04s0008g01960	Copper-transporting ATPase PAA2	AT5G21930
VIT_04s0008g01970	ER (ERECTA)	AT2G26330
VIT_04s0008g01980	MADS-box agamous-like 30	-
VIT_04s0008g01990	Myosin-like protein XI-I	AT4G33200
VIT_04s0008g02000	Unknown protein	AT5G21940
VIT_04s0008g02010	Endo-1,4-beta-glucanase	AT3G43860
VIT_04s0008g02020	Cellulase	AT3G43860
VIT_04s0008g02030	Unknown protein	AT2G26310
VIT_04s0008g02040	Heterotrimeric G protein alpha subunit	AT2G26300
VIT_04s0008g02050	Hydrolase, alpha/beta fold	AT4G33180
VIT_04s0008g02070	Avr9/Cf-9 induced kinase 1	AT2G05940
VIT_04s0008g02080	GCR1 (G-protein-coupled receptor 1)	AT1G48270
VIT_04s0008g02090	Copper transporter 5	AT1G72510
VIT_04s0008g02100	CID7 damaged DNA binding	AT2G26280
VIT_04s0008g02110	No hit	-

VIT_04s0008g02120	EMB2758 (embryo defective 2758)	AT4G33170
VIT_04s0008g02140	EMB2261 (embryo defective 2261)	AT4G33170
VIT_04s0008g02150	DCL3 (DICER-like 3)	AT3G43920
VIT_04s0008g02170	DCL3 (DICER-like 3)	AT3G43920
VIT_04s0008g02180	BRCT domain-containing protein	AT3G43930
VIT_04s0008g02190	Glutathione synthase S6 modification	-
VIT_04s0008g02200	3-beta-hydroxy-delta5-steroid dehydrogenase	AT2G26260
VIT_04s0008g02210	RPD1 (root primordium defective 1)	AT5G21970
VIT_04s0008g02220	Sterile alpha motif (SAM) domain-containing protein	AT2G45700
VIT_04s0008g02230	AP2 domain-containing transcription factor ORA47	AT1G19210
VIT_04s0008g02240	Ubiquitin thiolesterase	-
VIT_04s0008g02250	Beta-ketoacyl-CoA synthase	AT2G26250
VIT_04s0008g02260	Dimethylaniline monooxygenase (N-oxide forming) 2	AT1G19250
VIT_04s0008g02270	Hydroxyproline-rich glycoprotein	AT5G21280
VIT_04s0008g02280	Unknown protein	AT3G43540
VIT_04s0008g02290	ABI3-interacting protein 2	AT5G20910
VIT_04s0008g02300	Pyruvate dehydrogenase E1 beta subunit	AT5G50850
VIT_04s0008g02310	ABI3-interacting protein 2, AIP2	AT5G20910
VIT_04s0008g02320	Coatomer subunit beta	AT4G31480
VIT_04s0008g02330	Protein tyrosine phosphatase	AT5G10700
VIT_04s0008g02340	Exocyst subunit EXO70 protein	AT4G31540
VIT_04s0008g02650	Unknown protein	AT5G10620
VIT_04s0008g02660	Calmodulin-binding protein	AT2G43040
VIT_04s0008g02670	Cryptochrome DASH	AT5G24850
VIT_04s0008g02800	SAUR_D	AT2G24400
VIT_04s0008g02810	Chaperone protein dnaJ	AT2G24395
VIT_04s0008g02820	Glycosyltransferase family protein 47	-
VIT_04s0008g02830	Galactokinase like protein	AT4G16130
VIT_04s0008g02840	Avirulence induced gene (AIG)	AT2G24390
VIT_04s0008g02850	Proteasome 20S beta subunit A (PBA1) (PRCD)	AT4G31300
VIT_04s0008g02860	Cation transport protein chaC	AT4G31290
VIT_04s0008g02870	Transcription factor	AT4G31270
VIT_04s0008g02880	Extracellular ligand-gated ion channel	AT2G21080
VIT_04s0008g02890	Receptor kinase	AT4G31250
VIT_04s0008g02900	Protein disulfide isomerase	AT4G31240
VIT_04s0008g02910	Tassel serine threonine kinase 1	AT2G24370
VIT_04s0008g02920	Desiccation protein PCC13-62 precursor	AT1G47980
VIT_04s0008g02930	Oligouridylate binding protein 1B UBP1B	AT1G17370
VIT_04s0008g02950	DNA topoisomerase I	AT4G31210
VIT_04s0008g02960	CYP706A12	AT5G36110

VIT_04s0008g03150	S-adenosyl-L-methionine-dependent methyltransferase mraW	AT5G10910
VIT_04s0008g03160	G protein protein gamma subunit (AGG2)	-
VIT_04s0008g03170	Ubiquitin-specific protease 26 (UBP26)	AT3G49600
VIT_04s0008g03180	Unknown protein	AT4G20325
VIT_04s0008g03190	F-box family protein (FBX13)	AT4G33160
VIT_04s0008g03200	Lachrymatory factor synthase	AT4G32870
VIT_04s0008g03210	Lachrymatory factor synthase	AT4G32870
VIT_04s0008g03220	Lysophospholipase	AT5G11650
VIT_04s0008g03230	Unknown protein	AT5G25840
VIT_04s0008g03240	BAM2 (big apical meristem 2)	AT2G25790
VIT_04s0008g03250	Homeobox gene 8	AT4G32880
VIT_04s0008g03260	Thioredoxin domain containing 14	AT5G11640
VIT_04s0008g03270	GATA transcription factor 11	AT5G25830
VIT_04s0008g03280	No hit	-
VIT_04s0008g03290	Peptidyl-tRNA hydrolase 2	AT4G32900
VIT_04s0008g03300	SWIM zinc finger family (MAPKKK)	AT5G11620
VIT_04s0008g03310	Pentatricopeptide (PPR) repeat	AT1G11290
VIT_04s0008g03320	UVB-resistance protein	AT5G11580
VIT_04s0008g03330	Nucleoporin nup85	AT4G32910
VIT_04s0008g03340	No hit	-
VIT_04s0008g03350	Unknown protein	AT2G25800
VIT_04s0008g03360	F-box and leucine-rich repeat protein 20	-
VIT_04s0008g03370	YebC	AT2G25830
VIT_04s0008g03380	Carotenoid cleavage dioxygenase 8	AT4G32810
VIT_04s0008g03390	No hit	-
VIT_04s0008g03400	DREB sub A-4 of ERF/AP2 transcription factor	AT5G11590
VIT_04s0008g03410	Unknown protein	AT5G11600
VIT_04s0008g03420	Exostosin family protein	AT5G25820
VIT_04s0008g03430	Exostosin family	AT5G25820
VIT_04s0008g03440	Exosome complex exonuclease RRP46	AT3G46210
VIT_04s0008g03450	Lignostilbene-alpha, beta-dioxygenase and related enzymes	AT3G63520
VIT_04s0008g03460	Histidine kinase 1 AHK3	AT1G27320
VIT_04s0008g03470	Myb domain protein 109	-
VIT_04s0008g03480	Beta-carotene 15,15'-monooxygenase	AT3G63520
VIT_04s0008g03490	Ankyrin repeat protein	-
VIT_04s0008g03500	Ankyrin	AT1G10340
VIT_04s0008g03510	Lignostilbene-alpha, beta-dioxygenase and related enzymes	AT3G63520
VIT_04s0008g03520	Ring-H2 finger protein ATL4J	-
VIT_04s0008g03530	Ankyrin repeat	AT1G10340
VIT_04s0043g00680	No hit	-

VIT_04s0043g00690	ARR22 Type A	AT3G04280
VIT_04s0043g00700	PTAC3 (plastid transcriptionally active3)	AT3G04260
VIT_04s0043g00710	Hypoxia up-regulated 1 HSP70	AT4G16660
VIT_04s0043g00720	Transketolase	AT2G34590
VIT_04s0043g00730	formamidopyrimidine-DNA glycosylase 1	AT1G52500
VIT_04s0043g00740	Cytoplasmic FMR1 interacting protein	AT5G18410
VIT_04s0043g00750	No hit	-
VIT_08s0032g00450	No hit	-
VIT_08s0032g01110	Axial regulator YABBY2	AT1G08465
VIT_08s0032g01120	Pentatricopeptide repeat-containing protein	-
VIT_08s0032g01130	Caffeic acid methyltransferase	AT5G54160
VIT_08s0032g01140	Unknown protein	AT5G16280
VIT_08s0105g00260	Digalactosyldiacylglycerol synthase 1	AT3G11670
VIT_08s0105g00270	NC domain-containing protein	AT5G06370
VIT_08s0105g00280	Ribosomal protein S8e	AT5G06360
VIT_08s0105g00290	Zinc finger (C3HC4-type ring finger)	AT5G01450
VIT_08s0105g00300	Phospholipase C	AT3G08510
VIT_08s0105g00310	Rhodanese domain-containing protein	AT3G08920
VIT_08s0105g00330	Enhanced silencing phenotype 4 ESP4 symplekin	AT5G01400
VIT_08s0105g00340	NLI interacting factor (NIF)	AT3G55960
VIT_08s0105g00350	DnaJ homolog, subfamily B, member 4	AT3G08910
VIT_08s0105g00360	PHD finger protein alfin	AT5G05610
VIT_08s0105g00370	Myb family	AT2G01060
VIT_08s0105g00380	Leucoanthocyanidin dioxygenase	AT3G11180
VIT_08s0105g00390	Calcium-dependent protein kinase 13 CPK13	AT3G51850
VIT_08s0105g00400	GT-1-like transcription factor	AT2G38250
VIT_08s0105g00410	Transposase, IS4	AT5G41980
VIT_08s0105g00420	Unknown	-
VIT_10s0092g00490	CYP71A12	-
VIT_10s0092g00500	CYP71D10	AT5G25120
VIT_10s0092g00510	CYP71D10p	AT3G26310
VIT_10s0092g00520	Leucine-rich repeat family	-
VIT_10s0092g00560	Transducin protein	AT2G16405
VIT_10s0092g00570	Leucine-rich repeat family	AT1G56140
VIT_11s0016g01900	N-MYRISTOYLtransferase	AT5G57020
VIT_11s0016g01910	THO complex subunit 6	AT2G19430
VIT_11s0016g01920	EIF-4A3	AT1G54270
VIT_11s0016g01930	Diacylglycerol acyltransferase	AT2G19450
VIT_11s0016g01940	Unknown protein	AT2G19460
VIT_11s0016g01950	Casein kinase I delta	AT1G72710

VIT_11s0016g02380	1-aminocyclopropane-1-carboxylate oxidase 2 (ACO1)	AT2G19590
VIT_11s0016g02400	K+ efflux antiporter (KEA4)	AT2G19600
VIT_11s0016g02410	MYB divaricata	AT5G56840
VIT_11s0016g02420	UDP-N-acetylglucosamine O-acyltransferase protein	AT4G29540
VIT_11s0016g02430	Dual-specific kinase DSK1	AT3G13690
VIT_12s0055g00970	Pentatricopeptide repeat	AT2G15630
VIT_12s0055g00980	Peroxidase precursor	AT5G39580
VIT_12s0055g00990	Peroxidase	AT5G64120
VIT_12s0055g01000	Peroxidase	AT5G39580
VIT_12s0055g01010	Peroxidase	AT5G64120
VIT_12s0055g01020	Peroxidase	AT5G39580
VIT_12s0055g01030	Peroxidase	AT5G64120
VIT_14s0066g00920	Polyribonucleotide nucleotidyltransferase	AT5G14580
VIT_14s0066g00950	Isocitrate dehydrogenase, chloroplast precursor	AT5G14590
VIT_14s0066g00960	Glutaredoxin	AT5G40370
VIT_14s0066g00970	Anthranilate phosphoribosyltransferase, chloroplast precursor	AT5G17990
VIT_14s0066g00980	Unknown protein	AT5G62960
VIT_14s0066g00990	TRNA methyltransferase complex GCD14 subunit	AT5G14600
VIT_14s0066g01000	Phosphate/phosphoenolpyruvate translocator	AT3G01550
VIT_14s0066g01010	Myb domain protein 98	AT4G18770
VIT_14s0066g01020	DEAD box RNA helicase 1	AT3G01540
VIT_13s0019g01410	OBP3 (OBF-binding protein 3)	AT5G02460
VIT_13s0019g01430	Heat shock protein 70	AT5G02500
VIT_13s0019g01440	No hit	-
VIT_13s0019g01450	Unknown protein	AT3G04020
VIT_13s0019g01470	Geranylgeranyltransferase type I beta subunit	AT2G39550
VIT_13s0019g01490	C2 domain-containing protein	AT3G55470
VIT_13s0019g01510	Unknown protein	AT2G39690
VIT_13s0019g01530	Adaptor-related protein complex 3, beta 2 subunit	AT3G55480
VIT_13s0019g01570	Unknown protein	AT5G54440
VIT_13s0019g01590	Pentatricopeptide repeat-containing protein	-
VIT_13s0019g01600	No hit	-
VIT_13s0019g01610	XH/XS domain-containing protein	AT3G48670
VIT_13s0019g01620	No hit	-
VIT_13s0019g01640	Unknown protein	AT1G13790
VIT_13s0019g01650	Alpha-expansin 6 precursor	AT2G39700
VIT_13s0019g01670	Telomeric DNA binding protein 1	AT5G13820
VIT_13s0019g01700	Scarecrow transcription factor 14 (SCL14)	AT1G07530
VIT_13s0019g01710	Scarecrow transcription factor 14 (SCL14)	AT1G07530
VIT_13s0019g01740	Scarecrow transcription factor 14 (SCL14)	AT1G07530

VIT_13s0019g01780	Scarecrow transcription factor 14 (SCL14)	AT1G07530
VIT_13s0019g01790	Scarecrow transcription factor 14 (SCL14)	AT1G07530
VIT_13s0019g01810	Scarecrow transcription factor 14 (SCL14)	AT1G07530
VIT_13s0019g01820	Cell division protein methyltransferase FtsJ	AT5G13830
VIT_13s0019g01840	Cell division cycle 20-like protein 1	AT5G13840
VIT_13s0019g01860	Actin-related protein 5	AT3G12380
VIT_13s0019g01870	No hit	-
VIT_13s0019g01890	DVL11/RTFL8 (ROTUNDIFOLIA like 8)	AT2G39705
VIT_13s0019g01900	FK506-binding protein 4/5	AT3G55520
VIT_13s0019g01920	Laccase	AT5G60020
VIT_13s0019g01930	Laccase	AT5G60020
VIT_13s0019g01940	Laccase	AT5G60020
VIT_13s0019g02120	Zinc finger (C2H2 type) family	AT2G37740
VIT_13s0019g02130	Tropinone reductase	AT5G06060
VIT_13s0019g02140	Tropinone reductase	AT5G06060
VIT_13s0019g02150	Laccase	AT5G60020
VIT_13s0019g02160	Laccase	AT5G60020
VIT_13s0019g02170	Laccase	AT5G06060
VIT_13s0019g02180	Tropinone reductase	AT5G06060
VIT_13s0019g02190	No hit	-
VIT_13s0019g02200	Protein phosphatase 2CA AHG3 PP2CA	AT3G11410
VIT_13s0019g02210	Sterol 4-alpha-methyl-oxidase 1 (SMO1)	AT1G07420
VIT_13s0019g02220	No hit	-
VIT_13s0019g02230	PAP/25A associated domain containing protein	AT2G39740
VIT_13s0019g02240	Ribosomal protein S7 (RPS7B) 40S	AT3G02560
VIT_13s0019g03090	Heat shock protein class I (HSP17.8-CI)	-
VIT_13s0019g03100	Cis-zeatin O-beta-D-glucosyltransferase	AT1G22400
VIT_13s0019g03110	Heat shock protein 17.6 kDa class I	-
VIT_13s0019g03120	Glucosyltransferase-2	AT1G22400
VIT_13s0019g03130	Glucosyltransferase-2	AT1G22400
VIT_13s0019g03140	Heat shock protein 17.6 kDa class I	-
VIT_13s0019g03150	Membrane protein	-
VIT_13s0019g03160	Heat shock protein 17.6 kDa class I	-
VIT_13s0019g03170	Heat shock protein 16.9 kDa class I	AT3G46230
VIT_13s0019g03180	Unknown protein	AT5G05840
VIT_13s0019g03190	Zinc finger (C3HC4-type ring finger)	AT5G05830
VIT_13s0019g03200	Myb domain protein 109	AT3G55730
VIT_13s0019g03210	Lectin-like protein	AT5G01090
VIT_13s0019g03220	Proline transporter 1 (ProT1)	AT2G39890
VIT_13s0019g03230	Unknown protein	-

VIT_13s0019g03240	Syntaxin 18	AT1G51740
VIT_13s0019g03250	Auxin-independent growth promoter	AT2G37980
VIT_13s0019g03260	Ribosomal protein L35a (RPL35aC) 60S	AT1G07070
VIT_13s0019g03270	Phosphate translocator protein2, Plastidic	AT3G11320
VIT_13s0019g03280	LIM domain containing protein	AT3G55770
VIT_13s0019g03290	Unknown protein	AT2G39910
VIT_13s0019g03300	Glycosyl hydrolase family 17	-
VIT_13s0019g03310	Transposon protein	AT5G05800
VIT_13s0019g03320	Acid phosphatase class B	AT2G39920
VIT_13s0019g03330	Adenylosuccinate lyase	AT1G36280
VIT_13s0019g03340	No hit	-
VIT_13s0019g03350	Sedoheptulose-1,7-bisphosphatase (SBPase), Chloroplast	-
VIT_13s0019g03360	Laccase	-
VIT_13s0019g03370	Myb family	-
VIT_13s0019g03380	Coronatine-insensitive protein 1	AT2G39940
VIT_13s0019g03390	Unknown protein	AT2G39950
VIT_13s0019g03400	Signal peptidase complex subunit 2	AT2G39960
VIT_13s0019g03410	Peroxisomal membrane protein (PMP36)	AT2G39970
VIT_13s0019g03420	C2 domain-containing protein	AT1G07310
VIT_13s0019g03430	Anthocyanin 5-aromatic acyltransferase	AT2G39980
VIT_13s0019g03450	Unknown protein	AT3G55820
VIT_13s0019g03460	Homeodomain transcription factor 5	AT3G11260
VIT_13s0019g03470	Translation initiation factor eIF-3 subunit 5	AT2G39990
VIT_13s0019g03480	HAD superfamily hydrolase	AT3G45740
VIT_13s0019g03490	Zinc finger (CCCH-type) family protein	AT2G20280
VIT_13s0019g03510	Zinc finger (CCCH-type) family protein	AT2G20280
VIT_13s0019g03700	Lateral organ boundaries protein 1	AT1G07900
VIT_13s0019g03710	Lateral organ boundaries protein 1	AT1G07900
VIT_13s0019g03720	Lateral organ boundaries protein 11	AT2G28500
VIT_13s0019g03730	No hit	-
VIT_13s0019g03750	Lateral organ boundaries protein 11	AT2G28500
VIT_13s0019g03760	Lateral organ boundaries protein 11	AT2G28500
VIT_13s0019g03770	DNA-directed RNA polymerase subunit beta'	-
VIT_13s0019g03780	Lateral organ boundaries protein 11	AT2G28500
VIT_13s0019g03800	Lateral organ boundaries protein 1	AT1G07900
VIT_13s0019g03810	Lateral organ boundaries protein 1	AT1G07900
VIT_13s0019g03820	Lateral organ boundaries protein 11	AT2G28500
VIT_13s0019g03830	Lateral organ boundaries protein 11	AT2G28500
VIT_13s0019g03840	Lateral organ boundaries protein 1	AT1G07900
VIT_13s0019g03860	F-type H+-transporting ATPase d chain	AT3G52300

VIT_13s0019g03870	Substrate carrier, Mitochondrial	AT2G35800
VIT_13s0019g03880	DnaJ homolog, subfamily C, member 19	AT2G35795
VIT_13s0019g03890	Calmodulin binding protein	AT5G03040
VIT_13s0019g04110	Retrotransposon protein	-
VIT_13s0019g04120	Rhomboid	AT3G07950
VIT_13s0019g04130	AarF domain containing kinase	AT2G39190
VIT_13s0019g04140	LHCA1	AT3G54890
VIT_13s0019g04150	Receptor protein kinase CRINKLY4 precursor	AT2G39180
VIT_13s0019g04160	Protein kinase	AT1G16670
VIT_13s0019g04170	Para-aminobenzoate (PABA) synthase	AT2G28880
VIT_13s0019g04180	Aminodeoxychorismate synthase/glutamine amidotransferase	AT2G28880
VIT_13s0019g04190	Chorismate synthase 1, chloroplast precursor	AT1G48850
VIT_13s0019g04200	Patatin	AT3G54950
VIT_13s0019g04210	No hit	-
VIT_13s0019g04220	Tryptophan/tyrosine permease family	AT5G19500
VIT_13s0019g04230	V-type H+-transporting ATPase subunit G	AT3G01390
VIT_13s0019g04240	Protein disulfide-isomerase A1	AT5G60640
VIT_13s0019g04250	Unknown protein	AT5G14990
VIT_13s0019g04260	Monoglyceride lipase	AT5G19290
VIT_13s0019g04270	No hit	-
VIT_13s0019g04280	Aquaporin PIP2B	AT2G37170
VIT_13s0019g04290	No hit	-
VIT_13s0019g04300	Ribosomal protein L12 (RPL12A) 60S	AT2G37190
VIT_13s0019g04310	DCP2 (decapping 2)	AT5G13570
VIT_17s0000g05480	EMB2454 (embryo defective 2454)	AT1G18920
VIT_17s0000g05490	Lateral organ boundaries domain family protein (LBD27)	AT3G47870
VIT_17s0000g05500	Cysteine endopeptidase	AT3G47910
VIT_17s0000g05510	Pentatricopeptide (PPR) repeat-containing protein	AT1G74750
VIT_17s0000g05520	Calcium-dependent protein kinase 30 CPK30	AT1G18890
VIT_17s0000g05530	DnaJ homolog, subfamily B, member 4	AT3G47940
VIT_17s0000g05540	H (+)-ATPase 11 AHA11	AT5G62670
VIT_17s0000g05550	Proton-dependent oligopeptide transport (POT) family protein	AT5G62680
VIT_17s0000g05560	Proton-dependent oligopeptide transport (POT) family protein	AT5G28470
VIT_17s0000g05570	Receptor protein kinase	AT5G62710
VIT_17s0000g05580	Isopiperitenol dehydrogenase	AT2G47140
VIT_17s0000g05600	(-)-isopiperitenol dehydrogenase	AT2G47140
VIT_17s0000g05610	Isopiperitenol dehydrogenase	AT2G47140
VIT_17s0000g05620	Integral membrane HPP family protein	AT5G62720
VIT_17s0000g05630	Homeodomain leucine zipper protein HB-1	AT3G01470
VIT_17s0000g05640	Nitrate transporter 1:2	AT1G69850

VIT_17s0000g05650	Unknown protein	AT1G74730
VIT_17s0000g05660	Polygalacturonase GH28	AT1G23460
VIT_17s0000g05670	Polygalacturonase GH28	AT3G15720
VIT_17s0000g05680	Band 7 family	AT5G62740
VIT_17s0000g05690	Isochorismate synthase 1, chloroplast precursor	AT3G01280
VIT_17s0000g05700	Phosphoribosylanthranilate transferase	AT1G74720
VIT_17s0000g05810	WRKY DNA-binding protein 72	AT5G15130
VIT_17s0000g05820	Ubiquitin-conjugating enzyme E2 A	AT2G02760
VIT_17s0000g05830	Unknown protein	AT5G62550
VIT_17s0000g05840	Calmodulin binding IQD31 (IQ-domain 31)	AT1G74690
VIT_17s0000g05850	ATATH1 (ABC2 homolog1)	AT3G47730
VIT_17s0000g05860	ATATH6 (ABC2 homolog 6)	AT3G47780
VIT_17s0000g05870	Aldose 1-epimerase protein	AT3G47800
VIT_17s0000g05880	Calcineurin phosphoesterase	AT3G47810
VIT_17s0000g05890	Protein kinase APK1B	AT2G02800
VIT_17s0000g05900	Basic helix-loop-helix (bHLH) family	AT1G74500
VIT_17s0000g06090	Pentatricopeptide (PPR) repeat-containing protein	AT1G74580
VIT_17s0000g06100	Pentatricopeptide (PPR) repeat-containing protein	AT1G74600
VIT_17s0000g06110	Glutathione S-transferase 9 GSTU9	AT5G62480
VIT_17s0000g06120	Glutathione S-transferase 9 GSTU9	AT5G62480
VIT_17s0000g06130	Glutathione S-transferase 9 GSTU9	AT5G62480
VIT_17s0000g06140	Glutathione S-transferase 9 GSTU9	AT5G62480
VIT_17s0000g06150	Glutathione S-transferase 9 GSTU9	AT5G62480
VIT_17s0000g06170	Pentatricopeptide (PPR) repeat-containing	AT1G74630
VIT_17s0000g06180	Hydrolase, alpha/beta fold	AT1G74640
VIT_17s0000g06390	Pentatricopeptide (PPR) repeat-containing protein	AT1G59720
VIT_17s0000g06400	NAC domain containing protein 100	AT5G61430
VIT_17s0000g06410	MYB transcription factor MIXTA-like 2	AT3G01140
VIT_17s0000g06420	Galactosyl transferase GMA12/MNN10	AT1G18700
VIT_17s0000g06430	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	AT1G26550
VIT_17s0000g06440	Galactoside 2-alpha-L-fucosyltransferase	AT2G03220
VIT_17s0000g06450	Ribulose-phosphate 3-epimerase, chloroplast precursor	AT5G61410
VIT_17s0000g06460	Zinc finger (C3HC4-type ring finger)	AT1G74410
VIT_17s0000g06470	Pentatricopeptide (PPR) repeat-containing protein	AT5G61400
VIT_17s0000g06480	Pentatricopeptide (PPR) repeat-containing protein	-
VIT_17s0000g06490	MKK5	-
VIT_17s0000g06500	Pentatricopeptide (PPR) repeat-containing	AT5G66520
VIT_17s0000g06510	Exonuclease	AT5G61390
VIT_17s0000g06520	Timing of CAB expression 1	AT5G61380
VIT_17s0000g06530	No hit	-

VIT_17s0000g06540	Exonuclease	-
VIT_17s0000g06550	Exonuclease	-
VIT_17s0000g06560	Retrovirus Pol polyprotein from transposon TNT 1-94	AT3G29785
VIT_17s0000g06570	Timing of CAB expression 1 protein	AT5G61380
VIT_17s0000g06580	Vesicle transport v-SNARE 11	AT5G39510
VIT_17s0000g06590	Galactosyl transferase GMA12/MNN10	AT1G74380
VIT_17s0000g06600	No hit	-
VIT_17s0000g06610	Zinc finger (C3HC4-type ring finger)	AT1G18660
VIT_17s0000g06620	Protein kinase pto	AT5G61350
VIT_17s0000g06630	Unknown protein	AT5G61340
VIT_17s0000g06640	formin-2	AT2G25050
VIT_17s0000g06650	IBS1 (impaired in baba-induced sterility 1)	AT1G18670
VIT_17s0000g06940	LAP4 protein	AT5G07910

XP-CLR		
Gene stable ID	**Functional annotation**	**Arabidopsis homolog**
VIT_01s0011g00100	MADS-box APETALA 1	AT1G69120
VIT_01s0011g00110	SEPALLATA1	AT5G15800
VIT_01s0011g00120	Unknown protein	AT1G69160
VIT_01s0011g00130	Squamosa promoter-binding protein 6 (SPL6)	AT1G69170
VIT_01s0011g00140	CRABS CLAW	AT1G69180
VIT_01s0011g00150	Unknown protein	AT1G26330
VIT_01s0011g00160	Alpha-1,4-glucan-protein synthase	AT3G08900
VIT_01s0011g00170	Brassinosteroid-6-oxidase [Vitis vinifera]	AT5G38970
VIT_01s0011g00190	Brassinosteroid-6-oxidase [Vitis vinifera]	AT3G30180
VIT_01s0011g00210	Cytochrome b5 isoform Cb5-D	AT1G26340
VIT_01s0011g00230	Dihydropterin pyrophosphokinase /dihydropteroate synthase	AT4G30000
VIT_01s0011g00240	Fructokinase-2	AT1G69200
VIT_01s0011g00250	6-phosphogluconolactonase	AT1G13700
VIT_01s0011g00280	feronia receptor-like kinase	AT3G51550
VIT_01s0011g00290	Unknown protein	AT1G69210
VIT_01s0011g00300	SIK1 (serine/threonine kinase 1)	AT1G69220
VIT_01s0011g00340	Glycosyl hydrolase family 28 protein	AT1G78400
VIT_01s0011g00350	CYP78A5	AT1G13710
VIT_01s0011g00370	SP1L2 (SPIRAL2)	-
VIT_01s0011g00380	SP1L1 (SPIRAL1-like1)	AT3G29770
VIT_01s0011g00390	Asparagine synthase	AT2G03667
VIT_01s0011g00400	Nuclear transport factor 2 (NTF2)	AT5G60980
VIT_01s0011g00410	Nuclear transport factor 2 (NTF2)	AT1G13740
VIT_01s0011g00420	RPK1 (receptor-like protein kinase 1)	AT3G02130
VIT_01s0011g00550	Hydrolase, alpha/beta fold family	AT1G13820
VIT_01s0011g00570	Glucan endo-1,3-beta-glucosidase 3 precursor	-
VIT_01s0011g00580	Pentatricopeptide (PPR) repeat-containing protein	AT1G26460
VIT_01s0011g00590	Acclimation of photosynthesis to environment	AT5G46110
VIT_01s0011g00600	Acclimation of photosynthesis to environment	AT5G46110
VIT_02s0012g00820	Unknown	-
VIT_02s0012g00830	Expansin-like B1	AT4G17030
VIT_02s0012g00840	Pentatricopeptide (PPR) repeat-containing protein	AT1G08070
VIT_02s0012g00850	Splicing factor PWI domain-containing protein	AT1G31870
VIT_02s0012g00860	No hit	-
VIT_02s0012g00870	RNA-binding protein 10	AT3G54230
VIT_02s0012g01950	Photosystem II protein D1	-
VIT_02s0012g01960	Transcription factor jumonji (jmj)	AT5G46910
VIT_02s0012g02190	Cellulose synthase CSLD2	AT5G16910

VIT_02s0012g02200	No hit	-
VIT_02s0012g02210	No hit	-
VIT_02s0012g02220	Xyloglucan endotransglucosylase/hydrolase 30	AT1G32170
VIT_02s0109g00280	No hit	-
VIT_02s0109g00290	CYP76C6	-
VIT_02s0109g00300	CYP76B1	AT3G61040
VIT_02s0241g00120	Receptor protein kinase	AT4G22730
VIT_02s0241g00130	No hit	-
VIT_02s0241g00140	Calmodulin (A)	AT1G12310
VIT_02s0241g00150	No hit	-
VIT_02s0241g00160	Esterase/lipase/thioesterase family	AT4G12230
VIT_02s0241g00170	Zinc finger (C2H2 type) family	AT4G12240
VIT_03s0017g00760	E3 ubiquitin-protein ligase HUWE1	-
VIT_03s0017g00770	Diacylglycerol kinase 2	-
VIT_03s0097g00380	Monofunctional aspartokinase	AT5G13280
VIT_03s0097g00390	Unknown protein	AT1G33780
VIT_03s0110g00180	No hit	-
VIT_03s0110g00190	Cytochrome oxidase subunit 1	ATMG01360
VIT_03s0110g00200	Apocytochrome b	ATMG00220
VIT_04s0008g03610	Xylan synthase	AT1G27600
VIT_04s0008g03620	Catalytic	AT5G11560
VIT_04s0008g03630	Binding	AT5G11550
VIT_04s0008g03640	FAD-binding domain-containing protein	AT5G11540
VIT_04s0008g03650	Embryonic flower 1	-
VIT_04s0008g03660	Embryonic flower 1	AT5G11530
VIT_04s0008g03670	Tesmin/TSO1-like CXC domain-containing	AT4G29000
VIT_04s0008g06060	Unknown	-
VIT_04s0008g06070	Aberrant root formation protein 4 ALF4	AT5G11030
VIT_04s0008g06080	Unknown protein	AT5G11040
VIT_04s0008g06090	Pentatricopeptide (PPR) repeat	AT1G08070
VIT_04s0008g06130	KNAT2 (knotted1-like homeobox gene 3)	AT5G25220
VIT_04s0008g06140	No hit	-
VIT_04s0008g06150	No hit	-
VIT_04s0008g06160	Neurochondrin family protein	AT4G32050
VIT_04s0008g06170	Unknown protein	AT5G25265
VIT_04s0008g06180	Histone-lysine N-methyltransferase ATX1	AT2G31650
VIT_04s0008g06190	Polyprotein	-
VIT_08s0032g00290	RNA-binding region RNP-1	AT5G32450
VIT_08s0032g00300	Annexin A3	AT5G12380
VIT_08s0032g00310	Ubiquitin-conjugating enzyme E2 A	AT2G02760

VIT_08s0032g00320	Pigment defective 318 (PDE318)	AT1G80770
VIT_08s0032g00330	Pigment defective 318 (PDE318)	AT1G80770
VIT_08s0032g00340	No hit	-
VIT_08s0032g00350	No hit	-
VIT_08s0032g00360	N-6 Adenine-specific DNA methylase	AT3G58470
VIT_08s0032g00370	No hit	-
VIT_08s0032g00380	Myosin-like protein XIC	AT1G08730
VIT_08s0032g00390	Myosin-like protein	AT1G17580
VIT_08s0032g00400	Unknown	-
VIT_08s0032g00410	Myosin-like protein XIK	AT5G20490
VIT_08s0032g00420	Exostosin	AT4G38040
VIT_08s0032g00440	Syntaxin 1B/2/3/4	AT5G08080
VIT_08s0032g00450	No hit	-
VIT_08s0032g01110	Axial regulator YABBY2	AT1G08465
VIT_08s0032g01120	Pentatricopeptide repeat-containing protein	-
VIT_08s0032g01130	Caffeic acid methyltransferase	AT5G54160
VIT_08s0032g01140	Unknown protein	AT5G16280
VIT_08s0105g00260	Digalactosyldiacylglycerol synthase 1	AT3G11670
VIT_08s0105g00270	NC domain-containing protein	AT5G06370
VIT_08s0105g00280	Ribosomal protein S8e	AT5G06360
VIT_08s0105g00290	Zinc finger (C3HC4-type ring finger)	AT5G01450
VIT_08s0105g00300	Phospholipase C	AT3G08510
VIT_08s0105g00310	Rhodanese domain-containing protein	AT3G08920
VIT_08s0105g00330	Enhanced silencing phenotype 4 ESP4 symplekin	AT5G01400
VIT_08s0105g00340	NLI interacting factor (NIF)	AT3G55960
VIT_08s0105g00350	DnaJ homolog, subfamily B, member 4	AT3G08910
VIT_08s0105g00360	PHD finger protein alfin	AT5G05610
VIT_08s0105g00370	Myb family	AT2G01060
VIT_08s0105g00380	Leucoanthocyanidin dioxygenase	AT3G11180
VIT_08s0105g00390	Calcium-dependent protein kinase 13 CPK13	AT3G51850
VIT_08s0105g00400	GT-1-like transcription factor	AT2G38250
VIT_08s0105g00410	Transposase, IS4	AT5G41980
VIT_08s0105g00420	Unknown	-
VIT_08s0105g00430	Omega-3 fatty acid desaturase, chloroplast precursor	AT5G05580
VIT_08s0105g00440	Selenoprotein	AT5G58640
VIT_08s0105g00450	Transducin protein	AT5G05570
VIT_08s0105g00460	Acyl-CoA oxidase (ACX4)	AT3G51840
VIT_09s0002g00230	Pentatricopeptide (PPR) repeat-containing protein	AT3G18020
VIT_09s0002g00260	Unknown protein	-
VIT_09s0002g00280	Ubiquitin-conjugating enzyme E2 J2	AT5G50430

VIT_09s0002g00300	APUM23 (Arabidopsis PUMILIO 23)	AT1G72320
VIT_09s0002g00310	ATP synthase CF0 A subunit	AT5G60390
VIT_09s0002g00320	Pectinesterase PME3	AT3G14310
VIT_09s0002g00330	Pectinesterase PME1	AT1G53840
VIT_10s0003g04520	No hit	-
VIT_10s0003g04530	Cation: chloride symporter	AT1G30450
VIT_10s0042g00010	Strictosidine synthase	-
VIT_10s0042g00020	Strictosidine synthase	AT3G57030
VIT_10s0042g00720	ATP-dependent RNA helicase	-
VIT_10s0042g00760	No hit	-
VIT_10s0042g00770	Leucine-rich repeat receptor-like protein kinase 1	AT4G08850
VIT_10s0042g00780	Gag-pol polyprotein	-
VIT_10s0042g00790	Unknown	-
VIT_10s0042g00800	Proteasome 26S regulatory subunit (RPN2)	AT2G32730
VIT_10s0042g00950	Succinyl-CoA ligase alpha 1 subunit	AT5G23250
VIT_10s0042g00960	DNAJ heat shock N-terminal domain-containing protein	AT5G23240
VIT_10s0092g00470	SHR5-receptor-like kinase	AT1G56130
VIT_10s0092g00480	CYP71D10p	AT3G26330
VIT_10s0092g00490	CYP71A12	-
VIT_10s0092g00500	CYP71D10	AT5G25120
VIT_10s0092g00510	CYP71D10p	AT3G26310
VIT_10s0092g00520	Leucine-rich repeat family	-
VIT_10s0092g00560	Transducin protein	AT2G16405
VIT_10s0092g00570	Leucine-rich repeat family	AT1G56140
VIT_10s0092g00580	No hit	-
VIT_10s0092g00590	Leucine-rich repeat family	AT1G56140
VIT_10s0092g00690	Cysteine-rich receptor-like protein kinase 8	AT4G23160
VIT_10s0092g00780	F-type H+-transporting ATPase alpha chain	ATMG01190
VIT_10s0092g00790	Ribosomal protein S19	-
VIT_11s0016g01710	Myosin-like protein XIK	AT5G20490
VIT_11s0016g01720	Threonine synthase	AT4G29840
VIT_11s0016g01730	VIP3 (vernalization independence 3)	AT4G29830
VIT_11s0016g01740	Zinc finger (C2H2 type) family	AT2G19385
VIT_11s0016g01750	Unknown protein	AT4G26060
VIT_11s0016g01760	Cleavage and polyadenylation specificity factor 5	AT4G29820
VIT_11s0016g01770	MKK2	AT4G29810
VIT_11s0016g01780	HAB1 (homology toABI1)	AT1G72770
VIT_11s0016g01790	Unknown protein	AT4G29790
VIT_11s0016g01800	Protein kinase MK6	AT4G33080
VIT_11s0016g01810	Unknown protein	AT5G12010

VIT_11s0016g01820	Lactoylglutathione lyase	AT5G57040
VIT_11s0016g01830	Protein kinase	AT2G19410
VIT_11s0016g01840	No hit	-
VIT_11s0016g01850	Anthocyanidin-3-glucoside rhamnosyltransferase	AT5G49690
VIT_11s0016g01860	RPS2 (resistant to p. syringae 2)	AT4G26090
VIT_11s0016g01870	Dihydrolipoamide S-acetyltransferase	AT1G54220
VIT_11s0016g01890	Telomere repeat binding factor 1	AT1G72740
VIT_11s0016g01900	N-MYRISTOYLtransferase	AT5G57020
VIT_11s0016g01910	THO complex subunit 6	AT2G19430
VIT_11s0016g01920	EIF-4A3	AT1G54270
VIT_11s0016g01930	Diacylglycerol acyltransferase	AT2G19450
VIT_11s0016g01940	Unknown protein	AT2G19460
VIT_11s0016g01950	Casein kinase I delta	AT1G72710
VIT_11s0016g02380	1-aminocyclopropane-1-carboxylate oxidase 2 (ACO1)	AT2G19590
VIT_11s0016g02400	K+ efflux antiporter (KEA4)	AT2G19600
VIT_11s0016g02410	MYB divaricata	AT5G56840
VIT_11s0016g02420	UDP-N-acetylglucosamine O-acyltransferase protein	AT4G29540
VIT_11s0016g02430	Dual-specific kinase DSK1	AT3G13690
VIT_11s0016g03130	Ceramide glucosyltransferase	AT2G19880
VIT_11s0016g03140	ERD7 (EARLY-responsive TO dehydration 7)	AT3G21600
VIT_11s0016g03150	TRNA a64-2'-o-ribosylphosphate transferase	AT2G40570
VIT_11s0016g03160	ABC transporter B member 11	AT3G28345
VIT_11s0016g03170	Arabidopsis histidine phosphotransfer AHP4	AT3G16360
VIT_11s0016g03180	ABI1 (ABA insensitive 1)	AT4G26080
VIT_11s0037g01210	Eceriferum 1 (CER1 protein) Sterol desaturase	AT5G57800
VIT_11s0052g00160	ATP binding, related	AT4G29920
VIT_11s0052g00170	Armadillo-like helical domain-containing	AT3G28430
VIT_12s0055g01150	Brassinosteroid insensitive 1-associated receptor kinase 1	AT4G33430
VIT_12s0028g00920	Glutathione S-transferase 9 GSTF9	AT2G30860
VIT_12s0028g00930	Glutathione S-transferase 9 GSTF9	AT2G30860
VIT_12s0028g00940	Electron transfer flavoprotein alpha-subunit precursor (Alpha-ETF)	AT1G06660
VIT_12s0028g00960	Phytoene synthase, chloroplast precursor	AT5G17230
VIT_12s0028g00980	Myb family	AT2G40260
VIT_12s0028g01000	Unknown protein	AT4G19645
VIT_12s0028g01010	Unknown	-
VIT_12s0028g01020	No hit	-
VIT_12s0028g01030	Unknown	-
VIT_12s0028g01040	Protein kinase	AT3G57750
VIT_12s0028g01050	Helicase in vascular tissue and TAPETUM	AT2G30800
VIT_12s0028g01060	No hit	-

VIT_12s0028g01070	WD-repeat protein 26	AT5G08560
VIT_12s0028g01080	Photosystem II oxygen-evolving complex precursor, 23kda PSBP	AT1G06680
VIT_12s0028g01090	Reticulon family protein (RTNLB5)	AT3G10260
VIT_12s0028g01100	Aldo/keto reductase	AT1G06690
VIT_12s0028g01110	Phytochrome- interacting factor 5 PIL6	AT2G43010
VIT_12s0028g01120	Amine oxidase	AT2G43020
VIT_12s0028g01130	No hit	-
VIT_12s0028g01140	Pentatricopeptide (PPR) repeat-containing protein	AT3G59040
VIT_12s0055g00750	Pentatricopeptide (PPR) repeat-containing protein	AT3G62470
VIT_12s0055g00760	No hit	-
VIT_12s0055g00770	SWAP (Suppressor-of-White-APricot)	AT4G31200
VIT_12s0055g00780	VPS20.2 SNF7	AT5G09260
VIT_12s0055g00790	Clathrin assembly protein 3	AT4G02650
VIT_12s0055g00800	Arachidonic acid-induced DEA1	AT1G12090
VIT_12s0055g00810	Cationic peroxidase	AT4G25980
VIT_12s0055g00820	Serine carboxypeptidase II	AT5G42240
VIT_12s0055g00830	Methyltransferase	AT3G26410
VIT_12s0055g00840	Sucrose-6-phosphate phosphatase	AT2G35840
VIT_12s0055g00850	Nodulin	AT3G43660
VIT_12s0055g00860	Nodulin	AT1G76800
VIT_12s0055g00870	Nodulin	AT1G76800
VIT_12s0055g00890	No hit	-
VIT_12s0055g00900	RAE1 RNA export 1 homolog	AT1G80670
VIT_12s0055g00910	Kelch repeat-containing F-box protein	AT1G22040
VIT_12s0055g00920	Aspartate aminotransferase	AT2G13810
VIT_12s0055g00930	Heavy-metal-associated domain-containing protein	AT2G28660
VIT_12s0055g00940	Sulfate transporter 1.2	AT1G78000
VIT_12s0055g00950	Receptor-like kinase 902	AT2G26730
VIT_12s0055g00960	Unknown	-
VIT_12s0055g00970	Pentatricopeptide repeat	AT2G15630
VIT_12s0055g00980	Peroxidase precursor	AT5G39580
VIT_12s0055g00990	Peroxidase	AT5G64120
VIT_12s0055g01000	Peroxidase	AT5G39580
VIT_12s0055g01010	Peroxidase	AT5G64120
VIT_12s0055g01020	Peroxidase	AT5G39580
VIT_12s0055g01030	Peroxidase	AT5G64120
VIT_12s0057g00980	Phytochrome defective C (PHYC)	AT5G35840
VIT_14s0066g00920	Polyribonucleotide nucleotidyltransferase	AT5G14580
VIT_14s0066g00950	Isocitrate dehydrogenase, chloroplast precursor	AT5G14590
VIT_14s0066g00960	Glutaredoxin	AT5G40370

VIT_14s0066g00970	Anthranilate phosphoribosyltransferase, chloroplast precursor	AT5G17990
VIT_14s0066g00980	Unknown protein	AT5G62960
VIT_14s0066g00990	TRNA methyltransferase complex GCD14 subunit	AT5G14600
VIT_14s0066g01000	Phosphate/phosphoenolpyruvate translocator	AT3G01550
VIT_14s0066g01010	Myb domain protein 98	AT4G18770
VIT_14s0066g01020	DEAD box RNA helicase 1	AT3G01540
VIT_14s0066g01030	Tubulin gamma complex component 2	AT5G17410
VIT_14s0066g01040	Cytosine methyltransferase (DRM2)	AT5G14620
VIT_14s0066g01050	Glycogen synthase kinase 3 beta	AT5G14640
VIT_14s0066g01060	Polygalacturonase GH28	AT5G14650
VIT_14s0066g01070	Peptide deformylase, chloroplast precursor	AT5G14660
VIT_14s0066g01080	ADP-ribosylation factor A1B	AT5G14670
VIT_14s0066g01090	Myb domain protein 24	AT5G40350
VIT_14s0066g01100	Monodehydroascorbate reductase, cytoplasmic isoform 2	AT3G27820
VIT_14s0066g01110	Ribosomal protein L12-1, chloroplast (CL12-A) 50S	AT3G27830
VIT_14s0066g01120	PWWP domain-containing protein	AT5G40340
VIT_14s0066g01130	Universal stress protein A	AT5G14680
VIT_14s0066g01140	Unknown protein	-
VIT_14s0066g01150	Cinnamoyl-CoA reductase	AT5G14700
VIT_14s0066g01160	Unknown protein	AT5G14710
VIT_14s0066g01170	MAP4K alpha1	AT5G14720
VIT_14s0066g01180	Phospholipid-transporting ATPase	AT3G27870
VIT_14s0066g01190	Unknown protein	AT3G27880
VIT_14s0066g01200	Protein kinase beta-1 subunit 5'-AMP-activated	AT3G01510
VIT_14s0066g01210	Carbonic anhydrase, chloroplast precursor	AT3G01500
VIT_14s0066g01380	Calcium homeostasis regulator CHoR1	AT3G55250
VIT_14s0066g01390	Metal-dependent phosphohydrolase HD domain-containing protein	AT5G40270
VIT_14s0066g01590	NHL repeat-containing protein	AT1G70280
VIT_14s0066g01600	NHL repeat-containing protein	AT5G14890
VIT_14s0066g01610	Zinc finger (C3HC4-type ring finger)	AT5G40250
VIT_14s0066g01620	Hypoxia-responsive	AT3G48030
VIT_14s0066g01630	UVH3 (ultraviolet hypersensitive 3)	AT3G28030
VIT_14s0066g01640	Nodulin MtN21 family	AT5G40230
VIT_14s0066g01650	Nodulin MtN21 family	AT3G28050
VIT_14s0066g01660	DegP protease	AT5G40200
VIT_14s0066g01670	Alpha-dioxygenase	AT3G01420
VIT_14s0066g01680	No hit	-
VIT_14s0066g01690	Pathogen-inducible alpha-dioxygenase	AT3G01420
VIT_14s0066g01700	Calmodulin binding protein	AT5G40190
VIT_14s0066g01710	Leaf senescence protein	AT3G28150

VIT_14s0066g01720	Bromo-adjacency (BAH) domain-containing protein	AT3G48050
VIT_14s0066g01730	Cellulose synthase CSLC04	AT3G28180
VIT_14s0066g01740	Unknown protein	AT1G22270
VIT_14s0066g01840	SAG101 (senescence-associated gene 101)	AT5G14930
VIT_18s0001g14060	Transposon protein, CACTA, En/Spm sub-class	AT3G11290
VIT_18s0001g14070	Unknown	-
VIT_18s0001g14080	Diphthine synthase (DPH5)	AT4G31790
VIT_18s0001g14400	Peptidyl-prolyl cis-trans isomerase ROC5 (rotamase CYP 5)	AT4G34870
VIT_18s0001g14410	Unknown protein	AT1G30755
VIT_18s0001g14420	Unknown	-
VIT_18s0001g14430	Unknown	-
VIT_18s0001g14440	Molecular chaperone DnaJ	AT4G36040
VIT_18s0001g14450	Ferredoxin: nadp+ Oxidoreductase PETH	AT5G66190
VIT_18s0001g14620	Ribosomal protein S16	-
VIT_18s0001g14630	ATSYTB/NTMC2T1.2/NTMC2TYPE1.2/SYTB	AT1G20080
VIT_18s0001g14640	No hit	-
VIT_18s0001g14650	DNA-directed RNA polymerase I subunit A12	-
VIT_18s0001g14660	P-glycoprotein 13	AT1G27940
VIT_18s0001g14670	Rac-like GTP-binding protein RAC1	AT1G75840
VIT_18s0001g14680	Vacuolar protein sorting 35	AT1G75850
VIT_18s0001g14690	Protein kinase	AT1G77280
VIT_18s0001g14700	Unknown	-
VIT_18s0001g14710	Ketol-acid reductoisomerase precursor	AT3G58610
VIT_18s0001g14720	Ankyrin repeat family protein	-
VIT_18s0001g14730	Glutaredoxin	AT5G42150
VIT_18s0001g14740	Protein binding	-
VIT_18s0001g14860	SKP1	AT5G42190
VIT_18s0001g14870	Subtilisin-type protease precursor	AT1G20160
VIT_18s0001g14880	Unknown protein	AT4G22000
VIT_18s0001g14890	ABA-responsive element-binding protein 3 (AREB3)	-
VIT_18s0001g14900	La domain-containing protein	AT4G35890
VIT_18s0001g14910	Mannitol dehydrogenase	AT4G39330
VIT_18s0001g14920	Unknown protein	AT1G20180
VIT_18s0001g14930	Unknown protein	AT1G75980
VIT_18s0001g14940	Pentatricopeptide (PPR) repeat-containing	AT3G26540
VIT_18s0001g14950	EMB2170 (embryo defective 2170)	AT1G76980
VIT_18s0001g14960	Pentatricopeptide (PPR) repeat-containing	AT1G77010
VIT_18s0001g14970	Pentatricopeptide (PPR) repeat-containing	AT1G43980
VIT_18s0001g14980	3-methyl-2-oxobutanoate dehydrogenase	AT1G21400
VIT_18s0001g14990	Dual-specific kinase DSK1	AT3G13690

VIT_18s0001g15000	ACT domain containing protein (ACR4)	AT1G76990
VIT_18s0001g15010	F-box and leucine-rich repeat protein 1	AT1G77000
VIT_18s0001g15020	DnaJ homolog, subfamily A, member 4	AT1G77020
VIT_18s0001g15050	Protein phosphatase 2C	AT1G43900
VIT_18s0001g15190	flavin-containing monooxygenase, putative	AT1G48910
VIT_18s0001g15200	SIK1 (serine/threonine kinase 1)	-
VIT_18s0001g15220	Unknown protein	AT1G31130
VIT_18s0001g15230	Unknown	-
VIT_18s0001g15240	Blue (type 1) copper domain	AT2G02850
VIT_18s0001g15250	Unknown	-
VIT_18s0001g15260	Myb domain protein 52	AT1G17950
VIT_18s0001g15270	SCL1 (scarecrow-like 1)	AT1G21450
VIT_18s0001g15280	RNA exonuclease 1	AT5G25800
VIT_18s0001g15290	Ribosome maturation protein SDO1	AT1G43860
VIT_18s0001g15300	No hit	-
VIT_18s0001g15310	Thioredoxin M-type	AT3G15360
VIT_18s0001g15320	SEU3B protein	AT1G43850
VIT_18s0001g15330	SWEET1	AT1G21460
VIT_18s0001g15340	Pentatricopeptide (PPR) repeat-containing protein	-
VIT_18s0001g15350	Pentatricopeptide (PPR) repeat-containing protein	AT3G21470
VIT_18s0001g15360	Thylakoid lumenal 29.8 kDa protein	AT1G77090
VIT_18s0001g15370	Exostosin family protein	AT1G21480
VIT_18s0001g15380	No hit	-
VIT_18s0001g15390	Gaiacol peroxidase	AT4G25980
VIT_18s0001g15400	KOW domain-containing transcription factor family protein	AT4G08350
VIT_18s0001g15410	Alcohol dehydrogenase 1	AT1G77120
VIT_18s0001g15420	Auxin efflux carrier protein 6	AT1G77110
VIT_18s0001g15430	Alliin lyase	-
VIT_18s0001g15450	Alcohol dehydrogenase 3	AT1G77120
VIT_18s0001g15460	Stearyl acyl carrier protein desaturase	AT1G43800
VIT_18s0001g15470	Leaf senescence related protein-like	AT1G48880
VIT_18s0001g15510	Unknown	-
VIT_18s0001g15520	Leaf senescence protein	AT1G48880
VIT_18s0001g15530	Pentatricopeptide (PPR) repeat-containing	AT3G09040
VIT_18s0001g15620	Receptor kinase TRKe	AT3G47090
VIT_18s0001g15630	MAP kinase activating protein	AT1G77220
VIT_18s0001g15640	Pathogenesis-related	AT1G78780
VIT_18s0001g15650	Pathogenesis related protein	AT1G78780
VIT_18s0001g15660	Pathogen-related	AT1G78780
VIT_18s0001g15670	Cytoplasm protein	AT1G21370

VIT_18s0001g15680	Cellulase	AT4G24260
VIT_18s0001g15690	Endo-1,4-beta-glucanase	-
VIT_18s0001g15700	GLTP3 (glycolipid transfer protein 3)	AT3G21260
VIT_18s0001g15710	Electron carrier/ oxidoreductase	AT1G21350
VIT_18s0001g15720	Leucine Rich Repeat receptor-like kinase	AT3G24240
VIT_18s0001g15730	Dof zinc finger protein DOF3.5	AT3G52440
VIT_18s0001g15740	No hit	-
VIT_18s0001g15750	Protein kinase Xa21	AT3G47110
VIT_18s0001g15760	Copine BON3 (BONZAI 3)	-

Table S3 Significantly enriched functional categories for genes identified in sweep regions by CLR analysis of *vinifera* candidate genes, based on VitisNet functional annotations

Functional category	*P* value	Count in category	Count in comparison
Actin-driven movement	1.38E-04	4	26
Abiotic stress response	2.53E-04	6	85
Plant-pathogen interaction	5.07E-04	11	318
Nudix hydrolase family	2.64E-03	3	27
Alcohol dehydrogenase superfamily	4.31E-03	3	32
Monoterpenoid indole alkaloid biosynthesis	4.84E-03	4	66
Flower development	5.43E-03	7	204
Ribosome organization and biogenesis	5.94E-03	5	111
Peroxisome membrane organization and biogenesis	8.88E-03	2	14

Table S4 Significantly enriched functional categories for genes identified in sweep regions by CLR analysis of *sylvestris* candidate genes, based on VitisNet functional annotations

Functional category	*P* value	Count in category	Count in comparison
Stilbenoid biosynthesis	1.93E-50	24	45
Phytoalexin biosynthesis	1.12E-44	24	69
Phenylpropanoid biosynthesis	1.13E-34	26	224
ERF subfamily transcription factor	3.04E-10	7	56
Ethylene-mediated Signaling pathway	8.76E-06	7	248
Flavonoid biosynthesis	6.27E-03	3	127

Table S5 Functional categories were assigned to all candidate genes under selection detected by F_{ST} between wild and cultivated samples using the VitisNet functional annotations

Functional category	*P* value	Count in category	Count in comparison
HSP-mediated protein folding	2.08E-20	34	146
Protein processing in endoplasmic reticulum	2.75E-12	31	222
AS2 family transcription factor	1.59E-09	13	48
Temperature stress response	5.41E-06	11	66
Glycosyl transference	1.68E-05	11	74
Cytokinin inactivation by glycosylation	3.18E-05	6	21
Subtilase-mediated proteolysis	4.09E-05	13	111
Flavin-containing monooxygenase	1.74E-04	7	39
Metabolism single reactions	2.64E-04	15	169
MYB family transcription factor	8.30E-04	14	169
GRAS family transcription factor	8.40E-04	7	50
Folate biosynthesis	2.82E-03	2	3
Salicylic acid biosynthesis	2.82E-03	2	3
Nucleic acid catabolism	3.03E-03	3	10

Table S6 Gene expression analysis of genes within the sex determination region. The genes are listed with their functions. Comparisons in expression between sexes (M = male, F=female, H=hermaphrodite) are colored when significant, with the higher expressed sex indicated. Non-colored cells indicate results that were significant but not after multiple test correction. The two F_{ST} peaks are defined in the text.

Gene ID	**Peak**	**Functional_annotation**	**M vs. F**	**M vs H**	**F vs. H**
VIT_02s0154g00110	1#	Trehalose-6-phosphate phosphatase (AtTPPA)	F	H	-
VIT_02s0154g00120	1#	Unknown	-	-	-
VIT_02s0154g00130	1#	Exostosin (Xyloglucan galactosyltransferase KATAMARI 1)	F	-	F
VIT_02s0154g00140	1#	3-oxoacyl-[acyl-carrier-protein] synthase 3 A, cpl precursor	F	-	F
VIT_02s0154g00150	1#	PLATZ transcription factor	-	M	-
VIT_02s0154g00160	1#	FMO family protein	F	-	F
VIT_02s0154g00170	1#	flavin-containing monooxygenase 3	F	-	F
VIT_02s0154g00180	1#	flavin-containing monooxygenase 3	-	-	-
VIT_02s0154g00190	1#	flavin-containing monooxygenase 3	F	H	F
VIT_02s0154g00200	1#	Unknown protein	F	-	F
VIT_02s0154g00210	1#	WRKY DNA-binding protein 21	-	-	-
VIT_02s0154g00220	1#	Zinc finger (C2H2 type) family	-	-	-
VIT_02s0154g00230	2#	Phosphatidic acid phosphatase / PAP2	-	M	-
VIT_02s0154g00240	2	Oxysterol binding protein	-	-	-
VIT_02s0154g00250	2	Oxysterol binding protein	-	-	-
VIT_02s0154g00260	2	Nitrate transporter	F	-	-
VIT_02s0154g00270	2	No hit	-	-	-
VIT_02s0154g00280	2	Arachidonic acid-induced DEA1	-	-	-
VIT_02s0154g00290	2	Extensin	-	-	-
VIT_02s0154g00300	2#	Small nuclear ribonucleoprotein Sm D3	-	-	-
VIT_02s0154g00310	2#	Protease inhibitor/seed storage/lipid transfer protein (LTP)	-	H	H
VIT_02s0154g00320	2#	Protease inhibitor/seed storage/lipid transfer protein (LTP)	-	-	-
VIT_02s0154g00330	2#	Unknown protein	-	-	-
VIT_02s0154g00340	2#		Not detected as expressed in flowers		
VIT_02s0154g00350	2#	L-lactate dehydrogenase A	-	-	H
VIT_02s0154g00360	2#	No hit	-	M	-
VIT_02s0154g00370	2#	YbaK/prolyl-tRNA synthetase associated region	M	M	-
VIT_02s0154g00380	2#	Unknown	F	-	F
VIT_02s0154g00390	2#	Autophagy 8f (APG8f)	-	H	-
VIT_02s0154g00400	2#	Scarecrow transcription factor 6 (SCL6)	-	M	-

VIT_02s0154g00420	2#		Not detected as expressed in flowers		
VIT_02s0154g00430	2#		Not detected as expressed in flowers		
VIT_02s0154g00410	2#	Unknown protein	-	M	F
VIT_02s0154g00440	2#	Unknown protein	-	-	-
VIT_02s0154g00450	2#	Zinc knuckle	-	M	-
VIT_02s0154g00460	2#	Unknown protein	-	-	-
VIT_02s0154g00470	2#	No hit	-	-	-
VIT_02s0154g00480	2#	Heat shock protein MTSHP	-	H	H
VIT_02s0154g00490	2#	Heat shock 22 kDa protein mitochondrial	-	-	-
VIT_02s0154g00500	2#	VAP27-1 (VAMP/synaptobrevin-associated protein 27-1)	-	M	-
VIT_02s0154g00510	2#	SEC14 cytosolic factor	-	-	H
VIT_02s0154g00520	2#	Aspartyl protease	-	-	-
VIT_02s0154g00530	2#	Histidine triad nucleotide binding protein 3	-	-	-
VIT_02s0154g00540	2#	Protein arginine N-methyltransferase	-	M	-
VIT_02s0154g00550	2#	DnaJ homolog, subfamily C, member 11	-	-	-

#, with top 0.5% D_{xy} values

Table S7 Functional categories were assigned to all candidate genes under selection detected by F_{ST} between wine and table grapes using the VitisNet functional annotations

Functional category	*P* value	Count in category	Count in comparison
Serine catabolism	1.08E-10	6	6
Development Senescence	1.29E-07	9	39
Amino acid catabolism	6.14E-06	10	76
Valine, leucine, and isoleucine metabolism	1.04E-05	3	3
LUG family transcription factor	1.48E-05	4	8
Methane metabolism	2.24E-04	10	115
Transcriptional co-repression	3.36E-04	4	16
Alcohol dehydrogenase superfamily	6.11E-04	5	32
Transcription factor MTERF	9.33E-04	5	35
Glycerolipid catabolism	3.07E-03	4	28
Fatty acid metabolism	4.95E-03	6	72
Phenylalanine biosynthesis	4.97E-03	11	201
Pentatricopeptide domain family	5.14E-03	21	515
CPP family transcription factor	9.34E-03	2	7